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INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

<p>(51) International Patent Classification.<sup>6</sup> : C12N 15/82, 9/12, C07K 14/415, A01H 5/00</p>	<p>A1</p>	<p>(11) International Publication Number: <b>WO 97/43427</b> (43) International Publication Date: 20 November 1997 (20.11.97)</p>
<p>(21) International Application Number: PCT/EP97/02443 (22) International Filing Date: 13 May 1997 (13.05.97) (30) Priority Data: 9610044.1 14 May 1996 (14.05.96) GB (71) Applicant (for all designated States except US): NOVARTIS AG [CH/CH]; Scharzwaldallee 215, CH-4058 Basel (CH). (72) Inventors; and (75) Inventors/Applicants (for US only): DE VRIES, Sape, Cornelis [NL/NL]; Roghorst 192, NL-6708 KS Wageningen (NL). SCHMIDT, Eduard, Daniel, Leendert [NL/NL]; Callunastraat 25, NL-6813 ET Arnhem (NL). VAN HOLST, Gerrit, Jan [NL/NL]; De Gouw 8, NL-1602 DN Enkhuizen (NL). HECHT, Valerie, France, Gabrielle [NL/NL]; Kees Muldenweg 25, NL-6707 HA Wageningen (NL). (74) Agent: ROTH, Bernhard, M.; Novartis AG, Patent- und Markenabteilung, Klybeckstrasse 141, CH-4002 Basel (CH).</p>		<p>(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, TJ, TM, TR, TT, UA, UG, US, UZ, VN, ARIPO patent (GH, KE, LS, MW, SD, SZ, UG), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG).  <b>Published</b> <i>With international search report. Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i></p>
<p>(54) Title: PRODUCTION OF APOMICTIC SEED (57) Abstract  The present invention provides, <i>inter alia</i>, a method of producing apomictic seeds comprising the steps of: (i) transforming plant material with a nucleotide sequence encoding a protein the presence of which in a cell, or membrane thereof, renders said cell embryogenic, (ii) regenerating the thus transformed material into plants, or carpel containing parts thereof, and (iii) expressing the sequence in the vicinity of the embryo sac. The protein may be a leucine repeat rich receptor kinase which preferably is modified to the extent that the ligand binding domain is deleted or functionally inactivated.</p> <p style="text-align: right; font-style: italic;">close prior art BIT See is very different from applicants</p> <p style="text-align: left; font-style: italic;">Potential</p>		

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### Production of Apomictic Seed

The present invention relates to the production of genetically transformed plants. In particular the invention relates *inter alia* to a process for inducing apomixis, to the apomictic seeds which result from the process, and to the plants and progeny thereof which result from the germination of such seeds.

Apomixis, which is vegetative (non-sexual) reproduction through seeds, is a genetically controlled reproductive mechanism found in some polyploid non-cultivated species. The process is classified as gametophytic or non-gametophytic. In gametophytic apomixis - of which there are two types (apospory and diplospory), multiple embryo sacs which typically lack antipodal nuclei are formed, or else megasporogenesis in the embryo sac takes place. In adventitious embryony (non-gametophytic apomixis), a somatic embryo develops directly from the cells of the embryo sac, ovary wall or integuments. In adventitious embryony, somatic embryos from surrounding cells invade the sexual ovary, one of the somatic embryos out-competes the other somatic embryos and the sexual embryo and utilizes the produced endosperm.

Were apomixis to be a controllable and reproducible phenomenon it would provide many advantages in plant improvement and cultivar development in the case that sexual plants are available as crosses with the apomictic plant.

For example, apomixis would provide for true-breeding, seed propagated hybrids. Moreover, apomixis could shorten and simplify the breeding process so that selfing and progeny testing to produce and/or stabilize a desirable gene combination could be eliminated. Apomixis would provide for the use as cultivars of genotypes with unique gene combinations since apomictic genotypes breed true irrespective of heterozygosity. Genes or groups of genes could thus be "pyramided and "fixed" in super genotypes. Every superior apomictic genotype from a sexual-apomictic cross would have the potential to be a cultivar. Apomixis would allow plant breeders to develop cultivars with specific stable traits for such characters as height, seed and forage quality and maturity. Breeders would not be limited in their commercial production of hybrids by (i) a cytoplasmic-nuclear interaction to produce male sterile female parents or (ii) the fertility restoring

capacity of a pollinator. Almost all cross-compatible germplasm could be a potential parent to produce apomictic hybrids.

Finally, apomixis would simplify commercial hybrid seed production. In particular, (i) the need for physical isolation of commercial hybrid production fields would be eliminated; (ii) all available land could be used to increase hybrid seed instead of dividing space between pollinators and male sterile lines; and (iii) the need to maintain parental line seed stocks would be eliminated.

The potential benefits to accrue from the production of seed via apomixis are presently unrealized, to a large extent because of the problem of engineering apomictic capacity into plants of interest. The present invention provides a solution to that problem in that it provides the means for obtaining plants which exhibit the adventitious embryony type of apomixis.

According to the present invention there is provided a method of producing apomictic seeds comprising the steps of:

- (i) transforming plant material with a nucleotide sequence encoding a protein the presence of which in an active form in a cell, or membrane thereof, renders said cell embryogenic,
- (ii) regenerating the thus transformed material into plants, or carpel-containing parts thereof, and
- (iii) expressing the sequence in the vicinity of the embryo sac.

By "vicinity of the embryo sac" is meant in one or more of the following: carpel, integuments, ovule, ovule premordium, ovary wall, chalaza, nucellus, funicle and placenta. The skilled man will recognize that the term "integuments" also includes those tissues, such as endothelium, which are derived therefrom. By "embryogenic" is meant the capability of cells to develop into an embryo under permissive conditions. It will be appreciated that the term "in an active form" includes proteins which are truncated or otherwise mutated with the proviso that they initiate or amplify embryogenesis whether or not in doing this they interact with the signal transduction components that they otherwise would in the tissues in which they are normally present.

The term "plant material" includes protoplasts, isolated plant cells (such as stomatal guard cells) possessing a cell wall, pollen, whole tissues such as emerged radicle, stem, leaf, petal,

hypocotyl section, apical meristem, ovaries, zygotic embryo *per se*, roots, vascular bundle, pericycle, anther filament, somatic embryos and the like.

A further embodiment of the invention relates to a DNA molecule comprising a nucleotide sequence encoding a protein the presence of which in an active form in a cell, or membrane thereof, renders said cell embryogenic.

The said nucleotide sequence may be introduced into the plant material, *inter alia*, via a bacterial or viral vector, by micro-injection, by co-incubation of the plant material and sequence in the presence of a high molecular weight glycol or by coating of the sequence onto the surface of a biologically inert particle which is then introduced into the material.

Expression of the sequence may yield a protein kinase capable of spanning a plant cell membrane. Typically the kinase may be a leucine rich repeat receptor like kinase which has the capacity to auto-phosphorylate. The skilled man will recognize what is meant by the term "leucine rich repeat receptor like kinase". Examples of such proteins include *Arabidopsis* RLK5 (Walker, 1993), *Arabidopsis* RPS2 (Bent *et al.* 1994), Tomato CF-9 gene product (Jones *et al.* 1994), Tomato N (Whitham *et al.* 1994), *Petunia* PRK1 (Mu *et al.* 1994), the product of the *Drosophila* Toll gene (Hashimoto *et al.* 1988), the protein kinase encoded by the rice OsPK10 gene (Zhao *et al.* 1994), the translation product of the rice EST clone ric2976 and the product of the *Drosophila* Pelle gene (Shelton and Wasserman, 1993). Still further examples of such proteins include the TMK1, Clavatal, Erecta, and TMKL1 gene products from *Arabidopsis*, the Flightless-1 gene product from *Drosophila*, the TrkC gene product from pig, the rat LhCG receptor and FSH receptor, the dog TSH receptor, and the human Trk receptor kinase. The protein may comprise a ligand binding domain, a proline box, a transmembrane domain, a kinase domain and a protein binding domain. In many receptor kinases the extracellular (ligand binding) domain serves as an inhibitor of the kinase domain in the ligand-free state. This arrest is removed after binding of the ligand. Accordingly, in one embodiment of the invention the protein either lacks a ligand binding domain or the domain is functionally inactivated so that the kinase domain can be constitutively active in the absence of an activating signal (ligand). Whether or not the protein possesses a ligand binding domain - functional or otherwise, once expressed and incorporated into the plant cell membrane the protein binding domain is preferably located intra-cellularly.

In a preferred embodiment of the method, the said sequence further encodes a cell membrane targeting sequence. The sequence may be that which is depicted in SEQ ID Nos. 1, 2, 20, or 32, or it may be similar in that it is complementary to a sequence which hybridizes under stringent conditions with the said sequences and which encodes a membrane bound protein having kinase activity. By "similar" is meant a sequence which is complementary to a test sequence which is capable of hybridizing to the inventive sequence. When the test and inventive sequences are double stranded the nucleic acid constituting the test sequence preferably has a  $T_m$  within  $20^{\circ}\text{C}$  of that of the inventive sequence. In the case that the test and inventive sequences are mixed together and denatured simultaneously, the  $T_m$  values of the sequences are preferably within  $10^{\circ}\text{C}$  of each other. More preferably the hybridization is performed under stringent conditions, with either the test or inventive DNA preferably being supported. Thus either a denatured test or inventive sequence is preferably first bound to a support and hybridization is effected for a specified period of time at a temperature of between  $50$  and  $70^{\circ}\text{C}$  in double strength citrate buffered saline (SSC) containing  $0.1\%$  SDS followed by rinsing of the support at the same temperature but with a buffer having a reduced SSC concentration. Depending upon the degree of stringency required, and thus the degree of similarity of the sequences, at a particular temperature, - such as  $60^{\circ}\text{C}$ , for example - such reduced concentration buffers are typically single strength SSC containing  $0.1\%$  SDS, half strength SSC containing  $0.1\%$  SDS and one tenth strength SSC containing  $0.1\%$  SDS. Sequences having the greatest degree of similarity are those the hybridization of which is least affected by washing in buffers of reduced concentration. It is most preferred that the test and inventive sequences are so similar that the hybridization between them is substantially unaffected by washing or incubation in one tenth strength sodium citrate buffer containing  $0.1\%$  SDS.

Accordingly, further comprised by the present invention is a DNA sequence as depicted in SEQ ID NOS: 22, 24, 26, 28 and 30 or a sequence which is complementary to one which hybridizes under stringent conditions with the said sequences and which encodes a membrane bound protein having kinase activity.

The sequence may be modified in that known mRNA instability motifs or polyadenylation signals may be removed and/or codons which are preferred by the plant into which the sequence is to be inserted may be used so that expression of the thus modified sequence in the said plant may yield substantially similar protein to that obtained by expression of the unmodified sequence in the organism in which the protein is endogenous.

In order to obtain expression of the sequence in the regenerated plant (and in particular the carpel thereof) in a tissue specific manner the sequence is preferably under expression control of an inducible or developmentally regulated promoter, typically one of the following: a promoter which regulates expression of SERK genes *in planta*, the *Arabidopsis* ANT gene promoter, the promoter of the O126 gene from *Phalaenopsis*, the carrot chitinase DcEP3-1 gene promoter, the *Arabidopsis* AtChitIV gene promoter, the *Arabidopsis* LTP-1 gene promoter, the *Arabidopsis* bel-1 gene promoter, the petunia fbp-7 gene promoter, the *Arabidopsis* AtDMC1 promoter, the pTA7001 inducible promoter. The DcEP3-1 gene is expressed transiently during inner integument degradation and later in cells that line the inner part of the developing endosperm. The AtChitIV gene is transiently expressed in the micropylar endosperm up to cellularisation. The LTP-1 promoter is active in the epidermis of the developing nucellus, both integuments, seed coat and early embryo. The bel-1 gene is expressed in the developing inner integument and the fbb-7 promoter is active during embryo sac development. The *Arabidopsis* ANT gene is expressed during integument development, and the O126 gene from *Phalaenopsis* is expressed in the mature ovule.

It is most preferred that the sequence is expressed in the somatic cells of the embryo sac, ovary wall, nucellus, or integuments.

The endosperm within the apomictic seed results from fusion of polar nuclei within the embryo sac with a pollen-derived male gamete nucleus. It is preferred that the sequence encoding the protein is expressed prior to fusion of the polar nuclei with the male gamete nucleus.

The invention further includes a DNA, but preferably a recombinant DNA, comprising a sequence encoding a protein the presence of which in an active form in a cell, or membrane thereof, renders said cell embryogenic. Preferred is a DNA encoding a protein which is a leucine rich repeat receptor like kinase and comprises a ligand binding domain, a proline box, a transmembrane domain, a kinase domain and a protein binding domain, the ligand binding domain optionally being absent or functionally inactive.

In particular, the invention embodies a DNA comprising a DNA sequence encoding a N-terminal protein fragment having the following amino acid sequence: Gln Ser Trp Asp Pro Thr Leu Val Asn Pro Cys Thr Trp Phe His Val Thr Cys Asn.

A specific embodiment of the invention relates to a DNA comprising a DNA sequence encoding a protein having the sequence depicted in SEQ ID Nos. 3 or 21, or a protein substantially similar thereto which is capable of being membrane bound and which has kinase activity. By substantially similar is meant a pure protein having an amino acid sequence which is at least 90% similar to the sequence of the proteins depicted in SEQ ID No 3 below. In the context of the present invention, two amino acid sequences with at least 90% similarity to each other have at least 90% identical or conservatively replaced amino acid residues in a like position when aligned optimally allowing for up to 8 gaps with the proviso that in respect of each gap a total not more than 4 amino acid residues is affected. For the purpose of the present invention conservative replacements may be made between amino acids within the following groups:

- (i) Serine and Threonine;
- (ii) Glutamic acid and Aspartic acid;
- (iii) Arginine and Lysine;
- (iv) Asparagine and Glutamine;
- (v) Isoleucine, Leucine, Valine and Methionine;
- (vi) Phenylalanine, Tyrosine and Tryptophan
- (vii) Alanine and Glycine

In addition, non-conservative replacements may also occur at a low frequency. Accordingly, the invention further embodies a DNA comprising a DNA sequence encoding a N-terminal protein fragment having the following amino acid sequence: Val Xaa Gln Ser Thr Asp Pro Thr Leu Val Asn Pro Cys Thr Thr Phe His Val Thr Cys Asn, with Xaa being a variable amino acid, but preferably Leu or Val.

Especially preferred within the scope of the invention is a DNA comprising a DNA sequence encoding a N-terminal protein fragment having the following amino acid sequence: Val Xaa Gln Ser Thr Asp Pro Thr Leu Val Asn Pro Cys Thr Thr Phe His Val Thr Cys Asn Xab Xac Xad Xae Val Xaf Arg Val Asp Leu Gly Asn Xag Xah Leu Ser Gly His Leu Xai Pro Glu Leu Gly Xaj Leu Xak Xal Leu Gln, with Xaa to Xak representing variable amino acids, but preferably

Xaa = Leu or Val

Xab = Asn or Gln

Xac = Glu or Asp or His

Xad = Asn or His

Xae = Ser or Arg or Gln



Xaf = Ile or Thr  
Xag = Ala or Ser  
Xah = Glu or Asn  
Xai = Val or Ala  
Xaj = Val or Lys  
Xak = Lys or Glu  
Xal = Asn or His

It is preferred that the DNA further encodes a cell membrane targeting sequence, and that the protein encoding region is under expression control of a developmentally regulated or inducible promoter, such as, for example, a promoter which regulates expression of SERK genes *in planta*, the carrot chitinase DcEP3-1 gene promoter, the *Arabidopsis* AtChitIV gene promoter, the *Arabidopsis* LTP-1 gene promoter, the *Arabidopsis* bel-1 gene promoter, the petunia fbp-7 gene promoter, the *Arabidopsis* ANT gene promoter, or the promoter of the O126 gene from *Phalaenopsis*; the *Arabidopsis* AtDMC1 promoter, or the pTA7001 inducible promoter.

Particularly preferred embodiments of the said DNA include those depicted in SEQ ID Nos. 1, 2, 20 or 32, or those which are complementary to one which hybridizes under stringent conditions with the said sequences and which encode a membrane bound protein having kinase activity. As indicated above, the DNA may be modified in that known mRNA instability motifs or polyadenylation signals may be removed and/or codons which are preferred by the plant into which the DNA is to be inserted may be used so that expression of the thus modified DNA in the said plant may yield substantially similar protein to that obtained by expression of the unmodified DNA in the organism in which the protein is endogenous.

The invention still further includes a vector which contains DNA as indicated in the three immediately preceding paragraphs, plants transformed with the recombinant DNA or vector, and the progeny of such plants which contain the DNA stably incorporated, and/or the apomictic seeds of such plants or such progeny.

The recombinant DNA molecules of the invention can be introduced into the plant cell in a number of art-recognized ways. Those skilled in the art will appreciate that the choice of method might depend on the type of plant, i.e. monocot or dicot, targeted for transformation. Suitable methods of transforming plant cells include microinjection

(Crossway *et al.*, *BioTechniques* 4:320-334 (1986)), electroporation (Riggs *et al.*, *Proc. Natl. Acad. Sci. USA* 83:5602-5606 (1986), *Agrobacterium* mediated transformation (Hinchey *et al.*, *Biotechnology* 6:915-921 (1988)), direct gene transfer (Paszkowski *et al.*, *EMBO J.* 3:2717-2722 (1984)), ballistic particle acceleration using devices available from Agracetus, Inc., Madison, Wisconsin and Dupont, Inc., Wilmington, Delaware (*see, for example*, Sanford *et al.*, U.S. Patent 4,945,050; and McCabe *et al.*, *Biotechnology* 6:923-926 (1988)), and protoplast transformation/regeneration methods (*see* U.S. Patent No. 5,350,689 issued Sept. 27, 1994 to Ciba-Geigy Corp.). Also *see*, Weissinger *et al.*, *Annual Rev. Genet.* 22:421-477 (1988); Sanford *et al.*, *Particulate Science and Technology* 5:27-37 (1987)(onion); Christou *et al.*, *Plant Physiol.* 87:671-674 (1988)(soybean); McCabe *et al.*, *Bio/Technology* 6:923-926 (1988)(soybean); Datta *et al.*, *Bio/Technology* 8:736-740 (1990)(rice); Klein *et al.*, *Proc. Natl. Acad. Sci. USA*, 85:4305-4309 (1988)(maize); Klein *et al.*, *Bio/Technology* 6:559-563 (1988)(maize); Klein *et al.*, *Plant Physiol.* 91:440-444 (1988)(maize); Fromm *et al.*, *Bio/Technology* 8:833-839 (1990); and Gordon-Kamm *et al.*, *Plant Cell* 2:603-618 (1990)(maize).

Comprised within the scope of the present invention are transgenic plants, in particular transgenic fertile plants transformed by means of the aforescribed processes and their asexual and/or sexual progeny, which still contain the DNA stably incorporated, and/or the apomictic seeds of such plants or such progeny.

The transgenic plant according to the invention may be a dicotyledonous or a monocotyledonous plant. Such plants include field crops, vegetables and fruits including tomato, pepper, melon, lettuce, cauliflower, broccoli, cabbage, brussels sprout, sugar beet, corn, sweetcorn, onion, carrot, leek, cucumber, tobacco, alfalfa, aubergine, beet, broad bean, celery, chicory, cow pea, endive, gourd, groundnut, papaya, pea, peanut, pineapple, potato, safflower, snap bean, soybean, spinach, squashes, sunflower, sorghum, water-melon, and the like; and ornamental crops including Impatiens, Begonia, Petunia, Pelargonium, Viola, Cyclamen, Verbena, Vinca, Tagetes, Primula, Saint Paulia, Ageratum, Amaranthus, Anthirrhinum, Aquilegia, Chrysanthemum, Cineraria, Clover, Cosmo, Cowpea, Dahlia, Datura, Delphinium, Gerbera, Gladiolus, Gloxinia, Hippeastrum, Mesembryanthemum, Salpiglossis, Zinnia, and the like. In a preferred embodiment, the DNA is expressed in "seed crops" such as corn, sweet corn and peas etc. in such a way that the apomictic seed which results from such expression is not physically mutated or otherwise damaged in comparison with seed

from untransformed like crops. Preferred are monocotyledonous plants of the *Graminaceae* family involving *Lolium*, *Zea*, *Triticum*, *Triticale*, *Sorghum*, *Saccharum*, *Bromus*, *Oryzae*, *Avena*, *Hordeum*, *Secale* and *Setaria* plants.

More preferred are transgenic maize, wheat, barley, sorghum, rye, oats, turf and forage grasses, millet and rice. Especially preferred are maize, wheat, sorghum, rye, oats, turf grasses and rice.

Among the dicotyledonous plants *Arabidopsis*, soybean, cotton, sugar beet, sugar cane, oilseed rape, tobacco and sunflower are more preferred herein. Especially preferred are soybean, cotton, tobacco, sugar beet and oilseed rape.

The expression 'progeny' is understood to embrace both, "asexually" and "sexually" generated progeny of transgenic plants. This definition is also meant to include all mutants and variants obtainable by means of known processes, such as for example cell fusion or mutant selection and which still exhibit the characteristic properties of the initial transformed plant, together with all crossing and fusion products of the transformed plant material. This also includes progeny plants that result from a backcrossing, as long as the said progeny plants still contain the DNA according to the invention

Another object of the invention concerns the proliferation material of transgenic plants.

The proliferation material of transgenic plants is defined relative to the invention as any plant material that may be propagated sexually or asexually *in vivo* or *in vitro*. Particularly preferred within the scope of the present invention are protoplasts, cells, calli, tissues, organs, seeds, embryos, pollen, egg cells, zygotes, together with any other propagating material obtained from transgenic plants.

Parts of plants, such as for example flowers, stems, fruits, leaves, roots originating in transgenic plants or their progeny previously transformed by means of the process of the invention and therefore consisting at least in part of transgenic cells, are also an object of the present invention. Especially preferred are apomictic seeds.

A further object of the invention is a method of producing apomictic seeds, but preferably seeds that are of the adventitious embryony type, comprising the steps of:

- (i) transforming plant material with a nucleotide sequence encoding a protein the presence of which in an active form in a cell, or membrane thereof, renders said cell

embryogenic, but preferably a protein which is a protein kinase capable of spanning a plant cell membrane and capable of autophosphorylation.

- (ii) regenerating the thus transformed material into plants, or carpel-containing parts thereof, and
- (iii) expressing the sequence in the vicinity of the embryo sac.

The kinase protein being expressed by the DNA according to the invention is preferably a leucine rich repeat receptor like kinase and comprises a ligand binding domain, a proline box, a transmembrane domain, a kinase domain and a protein binding domain. In a specific embodiment of the invention, the said kinase protein may lack a functional ligand binding domain but comprises a proline box, a transmembrane domain, a kinase domain and a protein binding domain.

The genetic properties engineered into the transgenic seeds and plants described above are passed on by sexual reproduction or vegetative growth and can thus be maintained and propagated in progeny plants. Generally said maintenance and propagation make use of known agricultural methods developed to fit specific purposes such as tilling, sowing or harvesting. Specialized processes such as hydroponics or greenhouse technologies can also be applied. As the growing crop is vulnerable to attack and damages caused by insects or infections as well as to competition by weed plants, measures are undertaken to control weeds, plant diseases, insects, nematodes, and other adverse conditions to improve yield. These include mechanical measures such a tillage of the soil or removal of weeds and infected plants, as well as the application of agrochemicals such as herbicides, fungicides, gametocides, nematocides, growth regulants, ripening agents and insecticides.

Use of the advantageous genetic properties of the transgenic plants and seeds according to the invention can further be made in plant breeding which aims at the development of plants with improved properties such as tolerance of pests, herbicides, or stress, improved nutritional value, increased yield, or improved structure causing less loss from lodging or shattering. The various breeding steps are characterized by well-defined human intervention such as selecting the lines to be crossed, directing pollination of the parental lines, or selecting appropriate progeny plants. Depending on the desired properties different breeding measures are taken. The relevant techniques are well known in the art and include but are not limited to hybridization, inbreeding, backcross breeding, multiline breeding,

variety blend, interspecific hybridization, aneuploid techniques, etc. Hybridization techniques also include the sterilization of plants to yield male or female sterile plants by mechanical, chemical or biochemical means. Cross pollination of a male sterile plant with pollen of a different line assures that the genome of the male sterile but female fertile plant will uniformly obtain properties of both parental lines. Thus, the transgenic seeds and plants according to the invention can be used for the breeding of improved plant lines which for example increase the effectiveness of conventional methods such as herbicide or pesticide treatment or allow to dispense with said methods due to their modified genetic properties. Alternatively new crops with improved stress tolerance can be obtained which, due to their optimized genetic "equipment", yield harvested product of better quality than products which were not able to tolerate comparable adverse developmental conditions.

In seeds production germination quality and uniformity of seeds are essential product characteristics, whereas germination quality and uniformity of seeds harvested and sold by the farmer is not important. As it is difficult to keep a crop free from other crop and weed seeds, to control seedborne diseases, and to produce seed with good germination, fairly extensive and well-defined seed production practices have been developed by seed producers, who are experienced in the art of growing, conditioning and marketing of pure seed. Thus, it is common practice for the farmer to buy certified seed meeting specific quality standards instead of using seed harvested from his own crop. Propagation material to be used as seeds is customarily treated with a protectant coating comprising herbicides, insecticides, fungicides, bactericides, nematocides, molluscicides or mixtures thereof. Customarily used protectant coatings comprise compounds such as captan, carboxin, thiram (TMTD<sup>®</sup>), methalaxyl (Apron<sup>®</sup>), and pirimiphos-methyl (Actellic<sup>®</sup>). If desired these compounds are formulated together with further carriers, surfactants or application-promoting adjuvants customarily employed in the art of formulation to provide protection against damage caused by bacterial, fungal or animal pests. The protectant coatings may be applied by impregnating propagation material with a liquid formulation or by coating with a combined wet or dry formulation. Other methods of application are also possible such as treatment directed at the buds or the fruit.

It is thus a further object of the present invention to provide plant propagation material for cultivated plants, but especially plant seed that is treated with an seed protectant coating customarily used in seed treatment.

It is a further aspect of the present invention to provide new agricultural methods such as the methods exemplified above which are characterized by the use of transgenic plants, transgenic plant material, or transgenic seed according to the present invention.

To breed progeny from plants transformed according to the method of the present invention, a method such as that which follows may be used: plants produced as described in the examples set forth below are grown in pots in a greenhouse or in soil, as is known in the art, and permitted to flower. Pollen is obtained from the mature stamens and used to pollinate the pistils of the same plant, sibling plants, or any desirable plant. Similarly, the pistils developing on the transformed plant may be pollinated by pollen obtained from the same plant, sibling plants, or any desirable plant. Transformed progeny obtained by this method may be distinguished from non-transformed progeny by the presence of the introduced gene(s) and/or accompanying DNA (genotype), or the phenotype conferred. The transformed progeny may similarly be selfed or crossed to other plants, as is normally done with any plant carrying a desirable trait. Similarly, tobacco or other transformed plants produced by this method may be selfed or crossed as is known in the art in order to produce progeny with desired characteristics. Similarly, other transgenic organisms produced by a combination of the methods known in the art and this invention may be bred as is known in the art in order to produce progeny with desired characteristics.

Further comprised by the invention is a method of obtaining embryogenic cells in plant material, comprising transforming the material with a recombinant DNA sequence or a vector according to the invention, expressing the sequence in the material or derivatives thereof and subjecting the said material or derivatives to a compound which acts as a ligand for the gene product of the said sequence.

The invention further relates to a method of generating somatic embryos under *in vitro* conditions wherein the SERK protein is overexpressed ectopically.

The invention still further includes the use of the said DNA in the manufacture of apomictic seeds, in which use the sequence is expressed in the vicinity of the embryo sac.

In a specific embodiment of the invention the SERK gene may be expressed in transgenic plants such as, for example, an *Arabidopsis* plant, under the control of plant expression signals, particularly a promoter which regulates expression of SERK genes *in planta*, but preferably a

developmentally regulated or inducible promoter such as, for example, the carrot chitinase DcEP3-1 gene promoter, the *Arabidopsis* AtChitIV gene promoter, the *Arabidopsis* LTP-1 gene promoter, the *Arabidopsis* bel-1 gene promoter, the petunia fbp-7 gene promoter, the *Arabidopsis* ANT gene promoter, or the promoter of the O126 gene from *Phalaenopsis*; the *Arabidopsis* AtDMC1 promoter, or the pTA7001 inducible promoter.

The promoters of the DcEP3-1 and the AtChit IV genes may be cloned and characterized by standard procedures. The DcSERK coding sequence (SEQ ID No. 2) is cloned behind the DcEP3-1, the AtChit IV or the AtLTP-1 promoters and transformed into *Arabidopsis*. The ligation is performed in such a way that the promoter is operably linked to the sequence to be transcribed. This construct, which also contains known marker genes providing for selection of transformed material, is inserted into the T-DNA region of a binary vector such as pBIN19 and transformed into *Arabidopsis*. *Agrobacterium*-mediated transformation into *Arabidopsis* is performed by the vacuum infiltration or root transformation procedures known to the skilled man. Transformed seeds are selected and harvested and (where possible) transformed lines are established by normal selfing. Parallel transformations with 35S promoter-SERK constructs and the entire SERK gene itself are used as controls to evaluate over-expression in many cells or only in the few cells that naturally express the SERK gene. The 35S promoter-SERK construct may give embryo formation wherever the signal that activates the SERK-mediated transduction chain is present in the plant. A testing system based on emasculation and the generation of donor plant lines for pollen carrying LTP1 promoter-GUS and SERK promoter-bamase is established.

tissue  
specific  
promoter

constitutive

The same constructs (35S, EP3-1, AtChitIV, AtLTP-1 and SERK promoters fused to the SERK coding sequence) are employed for transformation into several *Arabidopsis* backgrounds. These backgrounds are wild type, male sterile, fis (allelic to emb 173) and primordia timing (pt)-1 lines, or a combination of two or several of these backgrounds. The wt lines are used as a control to evaluate possible effects on normal zygotic embryogenesis, and to score for seed set without fertilization after emasculation. The ms lines are used to score directly for seed set without fertilization. The fis lines exhibit a certain degree of seed and embryo development without fertilization, so may be expected to have a natural tendency for apomictic embryogenesis, which may be enhanced by the presence of the SERK constructs. The pt-1 line has superior regenerative capabilities and has been used to initiate the first stably embryogenic *Arabidopsis* cell suspension cultures. Combinations of several of the above backgrounds are obtained by

crossing with each other and with lines containing ectopic SERK expressing constructs. Except for the ms lines, propagation can proceed by normal selfing, and analysis of apomictic traits following emasculation. A similar strategy is followed in which the ATChilV, AtLTP-1 and SERK promoters are replaced by the bel-1 and fbp-7 promoters as well by other promoters specific for components of the female gametophyte.

*= tissue specific*

Additional constructs are generated that have constitutive receptor kinase activity. Most of the receptor kinases of the SERK type act as homodimeric receptors, requiring autophosphorylation before being able to activate downstream signal transduction cascades. In many receptor kinases the extracellular domain serves as an inhibitor of the kinase domain in the ligand-free stage. This arrest is removed after binding of the ligand (Cadena and Gill, 1992). By introduction of a SERK construct, from which the extracellular ligand-binding domain has been removed, mutant homodimeric (in cells that do not have a natural population of SERK proteins) or heterodimeric (in cells that also express the unmodified forms) proteins can be generated with a constitutively activated kinase domain. This approach, when coupled to one of the promoters active in the nucellar region, results in activation of the embryogenic pathway in the absence of the activating signal. This may be an important alternative in cases where it is necessary or desirable to have activation of the SERK pathway only dependant on specific promoter activity and independent of temporal regulation of an activating signal. Introduction of SERK constructs that result in fertilization-independent-embryogenesis (fie) are tested in other species for their effect. In order to recognize the fie phenotype, the skilled man will use appropriate male sterile backgrounds. However, pollination is often necessary for apomixis of the adventitious embryony type, in order to ensure the production of endosperm.

Whilst the present invention has been particularly described by way of the production of apomictic seed by heterologous expression of the SERK gene in the nucellar region of the carpel, the skilled man will recognize that other genes, the products of which have a similar structure/function to the SERK gene product, may likewise be expressed with similar results. Moreover, although the example illustrates apomictic seed production in *Arabidopsis*, the invention is, of course, not limited to the expression of apomictic seed-inducing genes solely in this plant. Moreover, the present disclosure also includes the possibility of expressing the SERK (or related) gene sequences in the transformed plant material in a constitutive - tissue non-specific manner (for example under transcriptional control of a CaMV35S or NOS promoter). In this case, tissue specificity is assured by the localized presence within the vicinity of the embryo



sac of the ligand of the product of the said gene. Furthermore, the SERK (or related) gene products may interact with proteins such as transcription factors which are involved in regulating embryogenesis. This interaction within tissue which has been transformed according to the present disclosure is also part of the present invention.

The skilled man who has the benefit of the present disclosure will also recognize that the SERK gene (and others as indicated in the preceding paragraph) may be transformed into plant material which may be propagated and/or differentiated and used as an explant from which somatic embryos can be obtained. Expression of such sequences in the transformed tissue (which is subjected to a ligand of the kinase gene products) substantially increases the percentage of the cells in the tissue which are competent to form somatic embryos, in comparison with the number present in non-transformed like tissue.

Plant material  
encourages  
cells to  
grow

The invention will be further apparent from the following description and the associated drawings and sequence listings.

SEQ ID NO. 1 depicts the *Daucus carota* genomic clone of the putative receptor kinase (SERK) associated with the transition of competent to embryogenic cells;

SEQ ID NO. 2 depicts the cDNA of the said putative kinase;

SEQ ID NOs. 3 depicts the the predicted protein sequence of the SERK protein encoded by the DNA of SEQ ID NO:1.

SEQ ID NOs: 4-16 depict the sequences of various PCR primers; and

SEQ ID NOs. 17-19 depict specific peptides contained within the gene product of SEQ ID NO. 2.

SEQ ID NO: 20 depicts the *Arabidopsis thaliana* partial genomic clone of the putative receptor kinase (SERK) associated with the transition of competent to embryogenic cells.

SEQ ID NO: 21 depicts the predicted protein sequence of the SERK protein encoded by the DNA of SEQ ID NO:20.

SEQ ID NOs: 22, 24, 26, 28 and 30 depict the partial DNA sequences of 5 EST clones with high homology to the SERK LRR sequences.

SEQ ID NOs. 23, 25, 27, 29 and 31 depict the predicted protein sequence of the partial DNA sequences of the 5 EST clones of SEQ ID Nos: 22, 24, 26, 28 and 30.

SEQ ID NO: 32 depicts the nucleotide sequence of the SERK cDNA from *Arabidopsis thaliana*.

SEQ ID NO: 33 depicts the predicted amino acid sequence of the SERK protein from *Arabidopsis thaliana* encoded by the DNA of SEQ ID NO: 32.

Figure 1 shows the results of an RT-PCR experiment performed on RNA extracted from the indicated tissues. 40 cycles followed by Southern blotting of the resulting bands is necessary to visualize SERK expression. Lanes include explants at day 7, treated for less (lane 1) or more (lane 2) then 3 days with 2,4-D. In the original a very faint signal is visible in lane 2, but not in lane 1. Established embryogenic cultures (lanes 4-6) but not a non-embryogenic control (lane 3) express the SERK gene. In carrot plants, no expression is detectable except for developing seeds after pollination (lane 7). Up to day 7 after pollination, the carrot zygote remains undivided, suggesting that the observed signal is coming only from the zygote. At day 10, the early globular and at day 20 the heart stage is reached in carrot zygotic embryogenesis. No signals are seen on Northern blots.

Figure 2A shows the results of a whole-mount *in situ* hybridization with the SERK cDNA on 7 day explants treated for 3 days with 2,4 D. Few cells on the surface of the explant express the SERK gene, and those cells that do are the ones that become embryogenic. Figure 2B shows a whole mount *in situ* hybridization on a partially dissected seed containing a globular zygotic embryo. Hybridization is visualized by DIG staining.

Figure 3 shows SERK expression in embryogenic hypocotyl cells during hormone-induced activation, determined by whole mount *in situ* hybridization. Bar: 50 mm

(A-E) Cell population generated by mechanical fragmentation of the activated hypocotyls. Only few of a certain type of cell; defined enlarged cell show SERK expression (asterisks). Small cytoplasmic cells (c), enlarging cells (eg) and large cells (l) never show SERK expression.

(F) Hypocotyl longitudinal section before hormone-induced activation. It is not possible to detect any SERK expression in any type of cell.

(G-I) Proliferating mass coming from the inner hypocotyl tissues 10 days after the beginning of the hormonal treatment (longitudinal section). In G a single enlarged cells showing SERK expression is detectable within a row of negative cells showing the same morphology. In H a single enlarged cell showing serk expression is detaching from the surface of the proliferating mass. In I a cluster of enlarged cells showing SERK expression is detectable at the surface of proliferating tissue.

(J) Proliferating mass coming from the inner tissues of the hypocotyl 10 days after the beginning of the rooting treatment (24 hours with 2,4-D followed by hormone removal). Both the root primordia and the enlarged cells detaching from the surface do not show any SERK expression.

Figure 4 shows the phenotype of Arabidopsis WS plants transformed with the 2200 bp SERK-luciferase construct at the seedling level. Pictures were taken at 28 days after germination of T2 seeds. In plant II and III no clear shoot meristem is visible at the seedling stage, 7 days after germination. The first two leaves, if they develop at all, are needleshaped as shown on the pictures taken 28 days after germination. At this time plant I, which shows no clear phenotype, already starts flowering. Secondary shoot meristems are already developing in plant no II and will also develop later from no III. Shoot meristems, inflorescences and normal flowers eventually develop on all plants.

Figure 5 shows how the 2200 bp SERK luciferase construct affects the number of developing ovules in the siliques of transformed plants.

Figure 6 shows autophosphorylation of purified SERK fusion protein *in vitro*. Lane 1: purified SERK fusion protein; Lane 2: serine phosphate; Lane 3: threonine phosphate; Lane 4: tyrosine phosphate.

The following description illustrates the isolation and cloning of the SERK gene and the production of apomictic seed by heterologous expression of the said gene in the nucellar region of the carpel so that somatic embryos form which penetrate the embryo sac and are encapsulated by the seed as it develops.

### **ISOLATION AND CLONING OF THE SERK GENE FROM *DAUCUS CAROTA***

#### **Isolation of cDNA clones that are preferentially expressed in embryogenic cell cultures of carrot**

In order to increase the chance of success for obtaining genes expressed in carrot suspension cells competent to form embryos, the number of embryo-forming cells as present in a series of established cell cultures was determined. A sub-population of cells that passed through a 30 mm nylon sieve was isolated from eight different cultures that ranged in age between 2 months and 4 years. In these sub 30 mm populations, the number of embryos formed from the single cells and small cell clusters was determined and expressed as a percentage of the total number of cells present at the start of embryogenesis. Sieved <30 mm cultures able to form somatic embryos with a frequency of more than 1% were then used as a source for competent cells, and cultures that produced less than 0.01% embryos were used as non-embryogenic controls. As main cloning strategies, cold plaque screening (Hodge *et al.* 1992) and differential display (dd) RT-PCR (Liang and Pardee, 1992) were used besides conventional differential screening of cDNA libraries.

Labeled probes for differential screening were obtained from RNA out of a <30 mm sieved sub-population of cells from either embryogenic or non-embryogenic cell cultures. Employing these probes in a library screen of approximately 2000 plaques yielded 26 plaques that failed to show any hybridization to either probe. These so-called cold plaques were purified and used for further analysis. From the total number of plaques that did hybridize, about 30 did so only with the probe from embryogenic cells. ddRT-PCR reactions using a combination of one anchor primer and one decamer primer were performed on mRNA isolated from three embryogenic, and three non-embryogenic suspension cultures. About 50 different ddRT-PCR fragments were obtained from each reaction. Using combinations of three different anchor and six different decamer primers, a total of approximately 1000 different cDNA fragments was visualized. Six of these PCR fragments were only found in lanes made with mRNA from <30 mm populations of cells from embryogenic cultures (Table 1) and with oligo combinations of the anchor primer (5'-TTTTTTTTTTGC-3') and the decamer primers (5'-GGGATCTAAG-3'), (5'-ACACGTGGTC-3'), (5'-TCAGCACAGG-3'). Because differential PCR fragments often consist of several unresolved cDNA fragments (Li *et al.* 1994), cloning proved to be essential prior to undertaking further characterization of the PCR fragments obtained.

All clones obtained were subjected to a second screen, that consisted of spot-dot Northern hybridization performed under conditions of high stringency. This method, that used RNA from entire unsieved embryogenic and non-embryogenic suspension cultures, proved to be a fast and reliable additional selection method. Only one clone (22-28) of the 30 clones obtained after differential screening, proved to be restricted to embryogenic cell cultures while the majority was constitutively expressed. The 26 clones obtained from the cold plaque screening required long exposure times in the spot-dot Northern analysis. Six of these clones failed to show any hybridization signal and 19 proved to be expressed in both embryogenic and non-embryogenic cell cultures. One clone (31-50) showed low expression in all embryogenic cultures, and in one non-embryogenic culture, but not in the others. Of the six cloned fragments obtained by ddRT-PCR display, four showed hybridization more or less restricted to transcripts present in embryogenic cultures. All clones that passed through the second screening were sequenced. Two of the ddRT-PCR clones (6-8 and 7-13) were identical to the carrot Lipid Transfer Protein (LTP) gene, previously identified as a marker for embryogenic carrot cell cultures. LTP expression is restricted to embryogenic cell clusters and the protoderm of somatic and zygotic embryos from the early globular stage onwards (Sterk *et al.* 1991). Therefore, while the LTP gene is not a marker for competent cells, its appearance in the screening confirms the validity of our methods with respect to the cloning of genes expressed early during somatic embryogenesis.

**cDNA clone 31-50 encodes a leucine-rich repeat containing receptor-like kinase**

The mRNA corresponding to the isolated clone 31-50 had an open reading frame of 1659 nucleotides encoding a protein with a calculated Mw of 55 kDa. Because clone 31-50 is mainly expressed in embryogenic cell cultures it was renamed Somatic Embryogenesis Receptor Kinase (SERK). The SERK protein contains a N-terminal domain with a five-times repeated leucine-rich motif that is proposed to act as a protein-binding region in LRR receptor kinases (Kobe and Deisenhofer, 1994). Between the extracellular LRR domain of SERK and the membrane-spanning region is a 33 amino acid region rich in prolines (13), that is unique for the SERK protein. Of particular interest is the sequence SPPPP, that is conserved in extensins, a class of universal plant cell wall proteins (Vamer and Lin, 1989). The proposed intracellular domain of the protein contains the 11 subdomains characteristic of the catalytic core of protein kinases. The core sequences HRDVKAAN and GTLGYIAPE in respectively the kinase subdomains VB and VIII suggest a function as a serine / threonine kinase (Hanks *et al.* 1988).

Another interesting feature of the intracellular part of the SERK protein is that the C-terminal 24 amino-acids resembles a single LRR. The serine and threonine residues present within the intracellular LRR sequence are surrounded by acidic residues and might be targets for the autophosphorylation of SERK, thereby regulating the ability of other proteins to interact with this receptor-kinase in a similar fashion as described for the SH2 domain of the EGF family of tyrosine receptor kinases.

Hybridization of the SERK cDNA clone to the carrot genome revealed the presence of only a single main hybridizing band after digestion with EcoR1, probably reflecting a single SERK gene in the carrot genome. This was confirmed after digestion with DdeI, an enzyme that cuts three times within the SERK gene. No signal was observed after Northern blotting of mRNA from embryogenic cell cultures and hybridization with labeled SERK probes, reflecting the low levels of transcript present in these cultures. Detection of the SERK transcript on the original spot-dot Northern was only possible after long exposure times compared with other probes.

The ability of the SERK protein to autophosphorylate was investigated *in vitro*, using a previously described autophosphorylation assay (Mu et al. 1994), with a bacterial fusion protein that contained the complete intracellular region of the SERK protein. The bacterially expressed SERK fusion protein was able to autophosphorylate, indicating that the SERK protein is able to fulfill a role as a protein kinase *in vivo* (Heldin, 1995).

#### **Expression of the SERK gene corresponds with the first appearance of competent cells during hypocotyl activation**

When carrot hypocotyls are induced with 2,4-D, only the cells of the provascular tissue proliferate. Cells of epidermal and cortical origin merely expand, suggesting that the provascular tissue derived cells form the newly initiated suspension culture. After removal of 2,4-D, the formation of somatic embryos occurs after 2-3 weeks. Somatic embryos are preceded by embryogenic cells, that are developed in turn from competent cells. While competent and embryogenic cell formation take place in the presence of 2,4-D, it was not clear when this occurred, and which cells acquired competence. Since previous experiments (Toonen et al. 1994) revealed that cell morphology is not a good criterion, the first appearance of single competent cells was determined experimentally by semi-automatic cell tracking performed on large populations of immobilized cells. Hypocotyl explants activated with 2,4-D for seven days were mechanically fragmented and samples of the resulting population of mainly single

suspension cells were immobilized to allow recording of their development by cell tracking. In the immobilized cell populations obtained in this way all the morphologically discernible cell types were present that were also seen in the un-fragmented activated hypocotyls. Because the different cell morphologies observed during hypocotyl activation were known (Guzzo et al. 1995), it was possible to trace back the original position of each type of cell in the activated explant. Small cytoplasm-rich cells (16x16 mm) are the proliferating cells that surround the vascular elements. Enlarging vacuolated cells (16x40 mm) are encountered on the surface of the mass of proliferating cells and these can detach from the surface when fully enlarged (35x90 mm). Large vacuolated cells (more than 60x140 mm) are the non-proliferating remnants of the hypocotyl epidermis and cortical parenchyma. The shape of the enlarging and fully enlarged cells could change from oval to elongate or triangular. Cell tracking on a total of 24,722 cells released from seven days activated hypocotyls showed that only 20 single cells formed a somatic embryo. Because of their dependance on continued 2,4-D treatment, the embryo-forming single cells are still in the competent cell stage. All of the embryo-forming single cells belonged to the category of 3,511 enlarged cells, that contained therefore competent cells in a frequency of 0.56%. The single cell tracking experiments clearly reveal that the ability of explant cells to reinitiate cell division under the influence of 2,4-D, resulting in a population of highly cytoplasmic and rapidly proliferating cells, does have a causal relation with the ability to become embryogenic. It is also clear that only a very limited number of the cells that make up the newly initiated embryogenic suspension culture are actually competent to form embryogenic cells.

Expression of the SERK gene, determined by whole mount *in situ* hybridization on a similar population of cells as used for the cell tracking experiments, was found to be restricted to only 0.44% of the enlarged cells. Therefore, the expression of the SERK gene appears closely correlated both qualitatively and quantitatively with the presence of competent single cells.

To obtain insight into the temporal regulation of SERK expression in the course of explant activation, whole mount *in situ* hybridization was performed on entire intact or hand-sectioned explants treated for different periods with 2,4-D. Representative samples were collected at daily intervals from explants untreated and treated for three days, six days, seven days or ten days with 2,4-D before returning to B5-0. No SERK-expressing cells were ever found in explants treated for less than three days with 2,4-D. While enlarged cells became present after the first five days of culture, the first few SERK-expressing enlarged cells were found after six-seven days of culture in the presence of 2,4-D treatment. These few cells were present at the surface

of the mass of proliferating cells originating from the provascular tissue. In the hypocotyls treated for ten days with 2,4-D, the number of SERK-positive cells had increased to 3.04% and included at this stage also cells present in small clusters. No SERK transcript was ever detected in small cytoplasm-rich cells or large vacuolated cells. Hypocotyls were also treated for only one day with 2,4-D and subsequently cultured in hormone-free medium for a total of seven or ten days. Under these conditions explant cells proliferated and gave rise to roots and non-embryogenic cell cultures, while SERK expression could never be detected. The in situ hybridization results described above were obtained from a relatively small number of explants and a few hundred cells, so RT-PCR followed by Southern hybridization was performed to obtain more quantitative results. These are shown in Figure 7 and confirm the close temporal correlation between the first appearance of competent cells in explants treated for three days with 2,4-D and the expression of the SERK gene. Northern hybridization never gave any signal after hybridization with SERK cDNA probes, not even after prolonged exposure in a Phosphorimager, in line with the extremely restricted expression pattern of the SERK gene.

**Expression of the SERK gene corresponds with the occurrence of competent cells in established embryogenic cell cultures**

While the results described so far indicate that competent and embryogenic cell formation is restricted to a particular class of enlarged cells during explant activation, the situation in an established embryogenic cell culture is more complex. Competent single cells in such cultures do not appear to belong to one cell type in particular, but have been shown to originate from all morphologically different cell types. In cell tracking experiments, embryogenic cells, that do not require exogenous auxin treatment, were never observed to be single but consisted of clusters of at least 3-4 cells (Toonen et al. 1994). SERK expression was found in all morphologically discernible single cell types that were present in an embryogenic cell culture at a frequency between 0.1 and 0.5% depending on the cell type. In non-embryogenic cultures, SERK expressing cells were never encountered. As was observed in the activated explants, SERK expression was not restricted to single cells, but also occurred in small clusters of 2 to 16 cells. Since clusters of this size are known to consist of embryogenic cells, these data show that SERK expression is not restricted to competent single cells, but may persist in small clusters of embryogenic cells. No SERK expression was encountered during the late globular, heart and torpedo-stages of somatic embryogenesis.



**The SERK gene is transiently expressed in zygotic embryogenesis**

The expression of the SERK gene in carrot plants was determined by RT-PCR. The results indicate that no SERK mRNA accumulates in any of the adult plant organs nor in flowers prior to pollination. The first occasion when SERK expression can be detected is in flowers at three days after pollination (DAP), at which stage fertilization has taken place and endosperm development has commenced. SERK mRNA remains present in flowers up to twenty DAP, corresponding with the early globular stage of the zygotic embryo (Yeung et al. 1996). Whole mount *in situ* hybridization on partially dissected carrot seeds confirmed that the SERK gene was only expressed in early embryos up to the globular stage. Expression was observed in the entire embryo including the suspensor. No expression was seen in seedlings, roots, stems, leaves, developing and mature flower organs, pollen grains and stigma's before and after fertilization. Tissues in the developing seed such as seed coat, integuments, all embryo sac constituents before fertilization as well as the endosperm at all stages of development investigated did not show any SERK expression. Later stages of carrot zygotic embryos were also completely devoid of SERK mRNA. Given this pattern of expression, that is restricted to the zygotic embryo, the signal as detected by RT-PCR in flowers at 3 and 7 DAP must come from SERK mRNA as present in zygotes, because in carrot the zygote remains undivided up to one week after pollination (Yeung et al. 1996). Although SERK expression persists to slightly later stages in zygotic globular embryos when compared to the somatic ones, these results confirm the transient pattern of expression as observed for the SERK gene during somatic embryogenesis and also imply that there is a correspondence between the formation of competent cells *in vitro* and the formation of the zygote *in vivo*.

**METHODS****Cell culture, hypocotyl explant induction and cell tracking**

Cell cultures were derived from *Daucus carota* cv. Flakkese and maintained as previously described (De Vries et al. 1988a). Cell suspension cultures were maintained at high cell density in B5 medium (Gamborg et al. 1968) supplemented with 2 mM 2,4-D (B5-2 medium). Embryo cultures with globular, heart and torpedo-stage somatic embryos were derived from <30 mm sieved cell cultures cultured at low cell density (100 000 cells / ml) in B5 medium without 2,4-D (B5-0). For hypocotyl explant induction experiments, plantlets were obtained from seed of

*Daucus carota* cv. S Valery as described previously (Guzzo *et al.*, 1994). The hypocotyls of one week old plantlets were divided in segments of 3-5 mm, incubated for various periods of time in B5-2 medium and returned to B5-0 medium. Seven days after explantation and exposure to 2,4-D the hypocotyl segments were fragmented on a 170 mm sieve and the resulting cells collected to form a fine cell suspension. Immobilization of these cells in B5-0.2 medium was performed in a thin layer of phytigel (Toonen *et al.* 1994). After one week of further culture 2,4-D was removed by washing the plates with B5-0 medium. This allowed embryos to develop beyond the globular stage. Recording the development of the immobilized cells was performed with a procedure modified from the previously described by Toonen *et al.* (1994). The main change involved a new MicroScan program for automatic 3-axis movement to scan all cells in the phytigel (Toonen *et al.* 1996).

#### **Nucleic acid isolation and analysis**

RNA was isolated from cultured cells and plant tissues as described by De Vries *et al.* (1988b). Poly(A)<sup>+</sup>-RNA was obtained by purification by oligo (dT) cellulose (Biolabs). For RNA gel blot analysis samples of 10 mg total RNA were electrophoresed on formamide gel, and transferred to nytran-plus membranes. For RNA spot-blot analysis 5 mg of total RNA was denatured and spotted onto nytran-plus filters using a hybridot manifold (BRL).

Genomic DNA was isolated according to Sterk *et al.* (1991). Samples of 10 mg genomic DNA were digested with different restriction enzymes and separated on agarose gel, and transferred to nytran-plus membrane (Schleicher & Schuell). Hybridization of RNA blots took place at 42°C in hybridization buffer containing 50% formamide, 6xSSC, 5xDenhardt, 0.5% SDS and 0.1 mg/ml salmon sperm DNA. Hybridization of DNA blots was performed as previously described (Sterk *et al.* 1991). Following hybridization, filters were washed under stringent conditions (3x20 min in 0.1% SSC, 1% SDS, at 65°C). Filters were exposed to Kodak X-Omat AR film. The integrity and the amount of RNA on the blots was confirmed by hybridization with an 18S ribosomal RNA probe. Nucleotide sequence analysis was performed on an ABI 373A automated DNA sequencer (Applied Biosystem).

#### **Screening procedures**

Two independent cDNA libraries were constructed with equal amounts of poly(A)<sup>+</sup>-RNA from total established cell cultures grown for six days in B5-2 medium, sieved <125 mm cell cultures grown for six days in B5-0 medium and sieved <30 mm cell cultures grown for six days in B5-0

medium. cDNA synthesis and cloning into the Uni-ZAP<sup>TM</sup> XR vector was performed according to the manufacturers protocol (Stratagene).

Differential screening of the cDNA libraries was performed essentially as described by Scott *et al.* (1991). RNA was isolated from either three embryogenic or three non-embryogenic cell cultures, that were grown for seven days in B5-2 after sieving through 30 mm mesh. First strand cDNA synthesis was performed on 4 mg total RNA using AMV reverse transcriptase (Gibco BRL). [<sup>32</sup>P]dATP labeled probes were prepared using random prime labeling on first strand cDNA. Pooled probes from embryogenic and non-embryogenic cell populations were hybridized to two pairs of nitrocellulose filters, each containing 1000 plaques from one cDNA library. After washing for 3x20 min in 0.1% SSC, 1% SDS at 65°C, hybridization was visualized by autoradiography for two days on Kodak X-omatic film. Plaques that only showed signal with the embryogenic transcript probe were purified by two further rounds of screening.

In order to identify cDNA clones which are expressed at low levels in the <30 mm sieved cell population, cold plaque screening was performed as described by Hodge *et al.* (1992). Plaques from the differential screening that did not show any signal after seven days of autoradiography were purified by two further rounds of screening. The resulting clones were used as probes for characterization of the expression pattern of the corresponding genes.

#### Differential Display RT-PCR

Differential display of mRNA was performed essentially as described by Liang and Pardee (1992). cDNA synthesis took place by annealing 1 mg of total RNA in 10 ml buffer containing 200 mM KCl, 10 mM Tris-HCl (pH 8.3), and 1 mM EDTA with 100 ng of one of the following anchor primers: (5'-TTTTTTTTTTCG-3'), (5'-TTTTTTTTTCTG-3'), (5'-TTTTTTTTTTCG-3'). Annealing took place by heating the mix for 3 min. at 83°C followed by incubation for 30 min at 42°C. Annealing was followed by the addition of 15 ml pre-warmed cDNA buffer containing 16 mM MgCl<sub>2</sub>, 24 mM Tris-HCl (pH 8.3), 8 mM DTT, 400 mM dNTP, and 4 Units AMV reverse transcriptase (Gibco BRL). cDNA synthesis took place at 42°C for 90 min. First strand cDNA was phenol/chlorophorm extracted and precipitated with ethanol using glycogen as a carrier. The PCR reaction was performed in a reaction volume of 20 ml containing 10% of the synthesized cDNA, 100 ng of anchor primer, 20 ng of one of the following 10-mer primers: (5'-GGGATCTAAG-3') , (5'-TCAGCACAGG-3'), (5'-GACATCGTCC-3'), (5'-CCCTACTGGT-3'), (5'-ACACGTGGTC-3'), (5'-GGTGACTGTC-3'), 2 mM dNTP, 0.5 Unit *Taq* enzyme in PCR buffer (10

mM Tris-HCl (pH 9.0), 1.5 mM MgCl<sub>2</sub>, 50 mM KCl, 0.01% gelatin and 0.1% Triton X100) and 6 nM [ $\alpha$ -<sup>32</sup>P] dATP (Amersham). PCR parameters were 94°C for 30 sec, 40°C for 1 min, and 72°C for 30 sec for 40 cycles using a Cetus 9600 (Perkin-Elmer). Amplified and labeled cDNAs were separated on a 6% denaturing DNA sequencing gel. Gels were dried without fixation and bands were visualized by 16 hours of autoradiography using Kodak X-omatic film. Bands containing differentially expressed cDNA fragments of 150-450 nucleotides were cut out of the gel and DNA was extracted from the gel slices by electroelution onto DE-81 paper (Whatmann). After washing of the paper in low salt buffer (100 mM LiCl<sub>2</sub> in 10 mM TE buffer), and elution of the cDNA in high salt buffer (1 M LiCl<sub>2</sub> in 10 mM TE buffer with 20% ethanol) the cDNA was concentrated by precipitation in ethanol using glycogen as carrier. Reamplification of the cDNA fragments using the same PCR cycling parameters as described above but PCR buffer containing 2.5 mM of both the 10-mer and the anchor oligo and 100 mM dNTP. DE-81 paper allowed an efficient recovery of the DNA fragments and reamplification generated an average of 500 ng DNA after 40 cycles. Amplified PCR products were blunt-ended using the Klenow fragment of *E.coli* DNA Polymerase I (Pharmacia), purified on Sephacryl-S200 columns (Pharmacia), ligated into a SmaI linearized pBluescript vector II SK (Stratagene) and transformed into *E.coli* using electroporation.

#### RT-PCR

Adult plant tissues from *Daucus carota* were obtained from S&G Seeds (Enkhuizen). Controlled pollination was performed by hand. Flower tissue RNA was obtained from three compete umbels for each time-point and contained all flower organs including pollen grains. 2 mg of total RNA from adult plant tissue or cell cultures was annealed at 42°C with 50 ng oligo (5'-TCTTGACCAGATAATTC-3') in 10 ml annealing buffer (250 mM KCl, 10 mM Tris-HCl pH 8.3, 1 mM EDTA). After 30 min. annealing, 1 unit AMV-reverse transcriptase was added in a volume of 15 ml cDNA buffer (24 mM Tris-HCl pH 8.3, 16 mM MgCl<sub>2</sub>, 8 mM DTT, 0.4 mM dNTP). The reverse transcription reaction took place for 90 min. at 42°C. PCR amplification of SERK-cDNA was carried out with two specific oligos for the SERK kinase domain, (5'-CTCTGATGACTTCCAGTC-3') and (5'-AATGGCATTTCATGG-3'). Amplification was carried out with 30 cycles of 30 sec. at 94°C, annealing at 54°C for 30 sec. and extension at 72°C for 1 min., followed by a final extension for 10 min. at 72°C.

#### **Whole mount *in situ* hybridization**

Whole mount *in situ* hybridizations were performed essentially as previously described (Engler et al. 1994). Cell cultures and somatic embryos were immobilized on poly-L-lysine coated glasses during fixation to improve handling. Whole mount *in situ* hybridization on explants took place by embedding hypocotyls from seven-days old plantlets in 3% Seaplaque agarose (Duchefa) and processing them in Eppendorf tubes. Transverse as well as longitudinal sections were made with a vibratome (Biorad Microcut). Sections of 50-170  $\mu$ m thick were incubated in B5-2 medium for a minimum of three days to induce formation of embryo-forming cells. Optimal induction was achieved with longitudinal hypocotyl sections with a thickness of at least 90  $\mu$ m. To obtain proliferating, non-embryogenic cell cultures, hypocotyl sections were exposed to 2,4-D for only 1 day, and subsequently transferred to B5-0 medium (Guzzo et al. 1994). Whole mount *in situ* hybridization on developing seeds was performed by removing the chalazal end of the seeds to allow easier probe penetration. After hybridization, the enveloping layers of integuments and endosperm were carefully removed to expose the developing embryos. *In situ* hybridization on sections was performed as described previously (Sterk et al. 1991) except for the use of non-radioactive probes.

All samples were fixed for 60 min. in PBS containing 70 mM EGTA, 4% paraformaldehyde, 0.25% glutaraldehyde, 0.1% Tween 20, and 10% DMSO. Samples were then washed, treated with proteinase K for 10 min, again washed and fixed a second time. Hybridization solution consisted of PBS containing 0.1% Tween 20, 330 mM NaCl, 50 mg/ml heparin, and 50% deionized formamide. Hybridization took place for 16 hours at 42°C using digoxigenin-labeled sense or antisense riboprobes (Boehringer Mannheim). After washing the cells were treated with RNaseA, and incubated with anti-digoxigenin-alkaline phosphatase conjugate (Boehringer Mannheim) which had been preabsorbed with a plant protein extract. Excess antibody was removed by washing followed by rinsing in staining buffer (100 mM Tris-HCl pH 9.5, 100 mM NaCl, 5 mM MgCl<sub>2</sub>, 1 mM levamisole) and the staining reaction was performed for 16 hours in a buffer containing NBT and BCIP. Observations were performed using a Nikon Optiphot microscope equipped with Nomarski optics.

#### **Autophosphorylation assay**

A 1.4 kB SspI cDNA fragment of the SERK cDNA encoding most of the open reading frame apart from the N-terminal three LRRs was cloned into the pGEX expression vector (Pharmacia).

A fusion protein consisting of SERK and the glutathione S-transferase gene product was synthesized by a three hours induction of transformed *E.coli* with 2 mM IPTG. Fusion protein was isolated and purified as described previously (Hom and Walker, 1994). Purified fusion protein was coupled to glutathione agarose beads (Sigma) and incubated for 20 min. at 20°C in a volume of 10 ml buffer: 50 mM Hepes (pH 7.6), 10 mM MgCl<sub>2</sub>, 10 mM MnCl<sub>2</sub>, 1 mM DTT, 1 mCi [ $\gamma$ -<sup>32</sup>P] (3 000 Ci/mmol) . Excess label was removed by washing the fusion protein/glutathione agarose beads three times for 5 min. in 50 mM Tris-HCl (pH 7.3), 10 mM MgCl<sub>2</sub> at 4°C. Protein was removed from the beads by cooking in SDS-PAGE loading buffer. Equal amounts of protein were separated by SDS-PAGE and protein autophosphorylation was visualized by autoradiography.

#### SERK fusion proteins produced with the Baculovirus expression system.

Further fusion proteins containing the intracellular part of the *Daucus carota* SERK protein (1.0 kB HindIII / SspI fragment of the carrot SERK cDNA clone 31-50) were made using the baculovirus vector pAHLT.

*In vitro* phosphorylation studies with this purified protein showed that most if not all of the autophosphorylation of this SERK fusion protein was at threonine residues (Figure 6)

#### Construction of viral transfer vectors

The pAHLT-B and pAHLT-C baculovirus transfer vectors were used for the cloning of two cDNA fragments of the carrot SERK gene. The SspI 1.41 kB fragment of carrot DcSERK cDNA was cloned into the SmaI site of pAHLT-B and the SspI / PvuII 1.07 kB fragment of carrot DcSERK cDNA was cloned into the SmaI site of pAHLT-C. The first construct contains the complete C-terminal part of the DcSERK protein and from the putative extracellular region the proline-rich region and three of the leucine-rich repeats. The second construct contains only the putative intracellular region of the DcSERK gene product. Nucleotide sequence analysis was performed in order to confirm the presence and the orientation of the DcSERK cDNA within the vector.

#### Transformation of insect cells

The resulting transfer vectors were used to transfect (lipofect) insect cell culture Sf21 from *Spodoptera frugiperda* in combination with linearized AcMNPV baculovirus DNA. Monolayers of Sf21 cells were transfected in 35 mm petridishes containing 2 ml of Hink's

medium. One microgram of linearized AcMNPV baculovirus DNA (Baculogold, Invitrogen) was added to 5 microgram of pAcHLT / SERK vector construct in 25 microliter of water. Fifteen microliter of Lipofectin (BRL) was mixed with 10 microliter of water, after which the DNA solution was added. After mixing 200 microliter of Hink's medium was added to the mix and the solution was transferred to the cell monolayer, from which the medium was removed. After one hour, 500 microliter of Hink's medium was added and the cells were incubated for another 3 hours. Finally, 1 ml of Hink's medium with 20% foetal bovine serum (FBS) was added and the cells were incubated for 4 days. After transfection, the viral infection could be identified by the reduced growth of cells, the swollen shape and the enlarged nucleus. After four days, infected cells were harvested and the medium containing infectious budded virus was collected and used for plaque assays and amplification of recombinant virus stocks.

#### Isolation of single recombinant viruses

Single recombinant virus plaques were isolated from monolayers of cells infected with a titration range of the primary virus stock. Infections were performed in 35 mm petridishes with monolayers of cells. Virus stocks were diluted in 600 microliter of Graces medium and added to the cell monolayer, followed by a 90 minutes incubation period at in Graces medium with 20% FBS. Afterwards, 3% Sea Plaque agarose was autoclaved, mixed with an equal amount of 2x Graces medium with 20% FBS and from the resulting agarose overlay solution 2 ml. was spread over the cell monolayers after removal of the viral inoculum. After 4 days of incubation single plaques could be visualized and purified for further analysis.

#### Fusion protein production.

After determining the titer of purified recombinant viruses, monolayers of Sf21 cells in 75 cm<sup>2</sup> flasks were infected with a multiplicity of infection (MOI) of 10. Incubation of cells with the virus inoculum was performed for 90 min. after which 8 ml. of Hink's medium with 10%FBS was added. After 3 days of incubation, cells were harvested and washed twice with PBS. Cells were lysed for 45 min on ice in twenty volumes of 1x insect cell lysis buffer (10 mM Tris pH 7.5, 130 mM NaCl, 1% Triton, 100 mM NaF, 10 mM NaPi, 10 mM NaPPi, with proteinase inhibitors: 16 mg/l benzamidine, 10 mg/l phenanthroline, 10 mg/l aprotinin, 10 mg/l leupeptin, 10 mg/l pepstatin A, 1 mM PMSF).

The lysate was cleared by centrifugation at 10.000 g for 30 min and the supernatant was batchwise incubated in TALON resin (with high affinity for the 6xHIS tag of the recombinant fusion protein). Binding was performed by gentle agitation for 20 min. at room temp. The resin was washed three times with lysis buffer, followed by an elution step with lysis buffer with 200 mM imidazole. Purified fusion protein was collected and purify and integrity was tested by SDS-PAGE.

#### Autophosphorylation assays

Protein kinase activity was determined by incubating 1 microgram of purified fusion protein for 30 min. at room temp. in a buffer containing 10 mM MgCl<sub>2</sub>, 10 mM MnCl<sub>2</sub>, 1 mM DTT and 10  $\mu$ M [gamma-32]ATP ( $10^5$  pm/pmol ATP). The autophosphorylated fusion protein was purified after SDS-PAGE from the gel in a buffer containing 50 mM NH<sub>4</sub>CO<sub>3</sub>, 0.1% SDS, 0.25% beta-mercaptoethanol. Protein was precipitated with 20  $\mu$ g/ml BSA and 20% (w/v) solid trichloroacetic acid. The precipitate was collected after centrifugation, hydrolysed in 50  $\mu$ l 6N HCl for 1 hour at 120 degrees Celcius. HCl was subsequently removed by lyophilization and the pellet was resuspended in a buffer consisting of 2.2% formic acid and 7.8% acetic acid. Hydrolysed protein was loaded onto cellulose thin layer chromatography plates together with control amino acid samples (phosphoserine, phosphothreonine, phosphotyrosine). Chromatography was performed in a buffer containing propionic acid: 1M ammonium hydroxide: isopropyl alcohol (90:35:35 v/v/v). After separation and drying of the plates, the separated amino-acids were visualized by spraying with 0.25% ninhydrin in acetone, followed by heating for 5 min. at 65 degrees Celcius. Plates were afterwards exposed to Phospho Imager cassettes in order to detect the phospho-labeled aminoacids.

#### SERK antibodies

Purified fusion proteins (10  $\mu$ g) were mixed in complete Freund adjuvant and injected IP into BALBc mice. After 4 weeks booster antigen was injected (10  $\mu$ g purified fusion protein in incomplete Freund adjuvant). Two weeks later a final booster was injected. One week after the final booster, serum was collected from these mice. The specificity and the titer of the resulting sera was tested on Western blots using total insect cell extracts with or without the SERK fusion proteins.



## INTRODUCTION OF THE SERK GENE INTO *PLANTA* AND THE PRODUCTION OF APOMICTIC SEED

### Carrot transformation with a SERK promoter fragment/luciferase gene fusion

The binary vector pMT500 is based on the pBIN19 vector (Bevan, 1984) and contains the firefly luciferase gene downstream of a polylinker containing 5 unique restriction sites was created by uni-directional ligation of the firefly luciferase coding region followed by the polyadenylation sequence from the pea *rbcS::E9* gene in the *HindIII*-*XbaI* site of the binary vector pMOG800 (kindly provided by Mogen N.V., Leiden, The Netherlands). The binary vector pMOG800 is based upon pBIN19 (Bevan, 1984) but while in pBIN19 the polylinker is flanked by the left border and the neomycin phosphotransferase (NPT II) expression cassette, the polylinker in pMOG800 is flanked by the right border and the NPT II expression cassette. From a genomic lambda clone, transcription regulating sequences from the carrot SERK gene were isolated by digestion with *HindIII* and *DraI* (SEQ ID No. 1), and cloned into the *HindIII* / *SmaI* sites of pBluescript SK+. From the resulting vector a *KpnI* / *SstI* fragment containing the SERK genomic DNA was isolated and cloned into the *KpnI* / *SstI* sites of the binary vector pMT500. The resulting DNA construct, pMT531, contained the 2200 bp genomic SERK DNA fragment as promoter sequence, the luciferase gene as vital reporter, and the E9 transcription terminator sequence.

The binary vector pMT531 was transformed by electroporation into *Agrobacterium tumefaciens* strains MOG101 and MOG301 (for transformation into carrot cells) and into *Agrobacterium tumefaciens* strain C58C1 (for transformation into *Arabidopsis thaliana* plants). Transformed colonies were selected on LB plates with 100mg/l kanamycin.

### Transformation of carrot cells

The firefly luciferase coding sequence under control of the genomic carrot *HindIII* / *DraI* 2200 bp DNA fragment was introduced into carrot cells by *Agrobacterium tumefaciens* mediated transformation of hypocotyl segments. Transformation of *Daucus carota* cv. 'Amsterdamse bak' was performed by slicing one week old dark grown seedlings into segments of 10 to 20 mm. Segments were incubated for 20 minutes in a freshly prepared 10 fold diluted overnight culture of *Agrobacterium*. The segments were dried and transferred to a modified Gamborgs B5 medium (P1 medium; S&G seeds, Enkhuizen, The Netherlands) supplemented with 2  $\mu$ M 2,4-D (P1-2) and solidified with agar (Difco, Detroit, Mi, USA). After two days of culture in the dark at  $25 \pm 0.5$  °C, segments were transferred to

solidified P1-2 medium supplemented with kanamycin ( $100 \text{ mg} \cdot \text{l}^{-1}$ ), carbenicillin ( $500 \text{ mg} \cdot \text{l}^{-1}$ ; Duchefa) and vancomycin ( $100 \text{ mg} \cdot \text{l}^{-1}$ ; Duchefa). After three weeks segments were transferred to fresh plates and transformed calli were selected after an additional three weeks. Transformed calli were grown on P1-2 plates with antibiotics for 3 weeks at a 16 hour light/8 hour darkness regime. Transformed embryogenic suspension cultures were initiated as described by transferring 0.2 g callus to 10 ml liquid P1-2 medium supplemented with  $200 \text{ mg} \cdot \text{l}^{-1}$  kanamycin,  $250 \text{ mg} \cdot \text{l}^{-1}$  carbenicillin and  $50 \text{ mg} \cdot \text{l}^{-1}$  vancomycin. During the first weeks 1 to 3 volumes of fresh medium were added to the culture at weekly intervals. After 5 to 7 weeks cultures were subcultured to a packed cell volume of 2 ml per 50 ml medium every two weeks and incubated at a 16 hour light / 8 hour darkness regime at  $25 \pm 0.5^\circ \text{C}$ .

One week after transfer to kanamycin selection medium, hypocotyl segments were sprayed with luciferin to test whether luciferase expression could be detected in transformed callus shortly after transformation. A large number of hypocotyl segments showed luciferase activity at the cut edges, but did not develop calli. Instead, growth of bacteria occurred, suggesting that the luciferase activity was of bacterial origin. Six to ten weeks after transformation, calli were obtained that showed luciferase activity in variable amounts, while no bacterial growth could be observed anymore. After 12 weeks, calli measuring 5 to 10 mm in diameter were used to start suspension cultures. At this time no bacterial contamination was observed. A control transformation experiment in which luciferase expression under influence of the CaMV 35S promoter was observed in single cells and cell clusters in the suspension culture demonstrating that the luciferase protein is active in *Daucus carota* suspension cultured cells.

#### Cell immobilisation

One-week old high-density ( $10^6 - 10^7 \text{ cells} \cdot \text{ml}^{-1}$ ) suspension cultures were sieved through nylon sieves with successive 300, 125, 50 and 30  $\mu\text{m}$  pore sizes (Monodur-PES; Verseidag Techfab, Walbeck, Germany). Single cells and cell clusters passing the last sieve are designated as  $< 30 \mu\text{m}$  populations. Control experiments with untransformed cells were performed with *Daucus carota* cv. 'Trophy' (S&G seeds) suspension cultures grown in P1-2 medium. Size fractionated cell populations smaller than 30  $\mu\text{m}$  were immobilised in phytigel (P8196; Sigma, St Louis, Mo, USA) in petriperm dishes (Heraeus, Hanau, Germany). The bottom layer consisted of 1 ml P1-0 medium with 5 mM  $\text{Ca}^{2+}$  and 0.2 % phytigel. Two

hundred thousand cells ( $< 30 \mu\text{m}$  and  $< 50 \mu\text{m}$  populations) in B5-0 medium without  $\text{Ca}^{2+}$  supplemented with 0.1 % phytigel were poured on top of the bottom layer. For this layer B5 was applied since, at room temperature, phytigel solidified in P1 medium without  $\text{Ca}^{2+}$ . After 2 hours of solidification an additional P1-0 layer with 0.2 % phytigel was poured onto the cell layer preventing the B5 layer to move. To prevent dehydration of the phytigel layers and to supply luciferin to the cells, 0.5 ml P1-0 medium containing  $0.05 \mu\text{M}$  luciferin (Promega, Madison, WI, USA) was added after solidification. The final luciferin concentration in the culture was  $0.02 \mu\text{M}$ . Luciferin detection on single cells was determined with a CCD camera for a period of 5 times one hour (Schmidt et al. (1997) Development 124: 2049-2062). After 7 days of culture, luciferin was removed from the cultures by extensive washing with P1-0 medium.

**Arabidopsis transformation with a SERK promoter fragment/luciferase gene fusion**

Wildtype WS plants were grown under standard long day conditions: 16 hours light and 8 hours dark.

The first emerging inflorescence was removed in order to increase the number of inflorescences. Five days later, plants were ready for vacuum infiltration.

Agrobacterium strain C58C1 containing the transformation plasmid was grown on a LB plate with 50 mg/l kanamycin, 50 mg/l rifampicin and 25 mg/l gentamycin. A single colony was used to inoculate 500 ml of LB medium containing 50 mg/l kanamycin, 50 mg/l rifampicin and 25 mg/l gentamycin. The cultures were grown O/N at 28 degrees Celsius and the resulting log phase culture ( $\text{OD}_{600} 0.8$ ) was centrifuged to pellet the cells and resuspended in 150 ml of infiltration medium (0.5x MS medium (pH 5.7) with 5% sucrose and  $10 \mu\text{l/l}$  benzylaminopurine). The inflorescences of 6 Arabidopsis plants are submerged in the infiltration suspension while the remaining parts of the plants (which are still potted) are placed upside down on meshed wire to avoid contact with the infiltration suspension.

Vacuum is applied to the whole set-up for 10 min. at 50 kPa. Plants are directly afterwards placed under standard long day conditions. After completed seed setting the seeds were surface sterilized by a 1% sodium hypochlorite soak, then thoroughly washed with sterile water and plated onto petridishes with 0.5xMS medium and 80 mg/l kanamycin in order to select for transformed seeds. After 5 days germination under long day conditions (10.000 lux), the transformed seedlings could be identified by their green color of their cotyledons

*transformation of plants*

(the untransformed seedlings turn yellow), and were further grown in soil under C1 lab conditions under long day conditions. This vacuum infiltration method resulted in approximately 0.1% transformed seeds.

Transformation of a construct containing both a gene encoding kanamycin resistance and the 2200 bp (HindIII / DraI) SERK genomic DNA fused to the firefly luciferase gene into *Arabidopsis thaliana* (WS) by vacuum infiltration resulted in six different kanamycin-resistant primary transformants (I, II, III, IV, V and VI). Plants IV and VI died at the seedling stage, although they were kanamycin resistant. A T2 generation could be obtained from the four plants I, II, III and V (Figure 4). Within the siliques of the T2 generation of plants no. III and V, an early inhibition in development could be observed in approximately 25-50 % of the seeds. The plants I and II did not show a reduction in the number of developing seeds.(Figure 5). Similar results were observed in a T3 generation, in which again approximately 25-50% of the seeds showed an early inhibition of normal seed development.

#### **Arabidopsis transformation with a AtSERK gene**

##### **Isolation of the AtSERK genomic and cDNA clones**

Using the DcSERK cDNA sequence (seq ID no. 2) as a probe, a lambda ZipLox genomic library made from *Arabidopsis Landsberg erecta* total genomic DNA is screened for the presence of homologous sequences. Three different lambda clones with inserts of 14, 18 and 20 kb respectively are obtained. The 14 kb clone is digested by EcoRI and the resulting fragments subcloned into pBluescript vectors. Fragments spanning the entire coding sequence of the AtSERK gene are isolated, sequenced and compared with the *Daucus* homologues. The resulting sequence is shown as SEQ ID NO: 20.

Using the DcSERK cDNA sequence (SEQ ID NO: 2) as a probe, a lambda ZAPII cDNA library is screened for the presence of homologous sequences. Four lambda clones are obtained and their inserts subcloned into pBluescript vectors using the helper phage excision procedure. Fragments spanning the entire AtSERK cDNA coding sequence of the AtSERK gene are isolated, sequenced and compared with the *Daucus* homologues. The resulting sequence is shown as SEQ ID NO: 32.

#### Plasmids containing promoter sequences

*Arabidopsis thaliana* LTP1 promoter fragment is obtained from the binary plasmid pUH1000 (Thoma, S., Hecht, U., Kipper, A., Borella, J., De Vries, S.C., Sommerville, C. (1994) Plant Physiol. 105, 35-45) by digestion with *Bam*H1 and *Hind*III and cloning into pBluescript SK<sup>-</sup> (pMT121).

- The CaMV 35S promoter enhanced by duplication of the -343 to -90 region (Kay *et al.*, (1987) Science 236: 1299-1302) is isolated from the pMON999 vector by digestion with *Hind*III and *Sst*I and cloned into the pBluescript SK<sup>-</sup> vector (pMT120).

- The promoter AtDMC1 (Klimyuk and Jones (1997) Plant Journal 11: 1-14).

Plasmid SLJ 9691 is a construct consisting of pBluescript SK<sup>+</sup> in which the *Arabidopsis thaliana* DMC1 genomic clone (accession number U76670) is cloned into the *Eco*RV site. SLJ 9691 carries *Eco*RV fragments of the 5' end of the AtDMC1 gene with the following modification: a *Bgl*II site instead of the second *Hpa*I site, two ATG codons in the first exon and an *Xho*I site at the ATG codon of the second exon.

- The FBP7 promoter from Petunia (Angenent *et al.* (1995) Plant Cell 7: 1569-1582).

The promoter of the FBP7 gene is cloned by subcloning the 0.6 kb *Hind*III - *Xba*I genomic DNA fragment of FBP7 into the *Hind*III - *Xba*I site of pBluescript KS<sup>-</sup>, resulting in the vector FBP201.

The pAtSERK binary vector constructs.

Based on the pBIN 19 vector, a binary vector pAtSERK is constructed for transformation of the *Arabidopsis thaliana* SERK cDNA under the control of different promoters.

The full length *Arabidopsis thaliana* cDNA clone of SERK (Seq ID No. NEW) is obtained from a pBluescript SK<sup>-</sup> plasmid. A *Sma*I - *Kpn*I 2.1 kb fragment containing the AtSERK cDNA is cloned into pBIN19 *Sma*I - *Kpn*I. The polyadenylation sequence from the pea *rbcs::E9* gene (Millar *et al.*, 1992), Plant Cell 4: 1075-1087) is placed downstream from the AtSERK cDNA by cloning a Klenow-filled *Eco*RI - *Hind*III E9 DNA fragment into the Klenow-filled *Xma*I site of the pBIN19:AtSERK vector in order to generate the binary vector pAtSERK.

#### Construction of plant expression vectors

The pAtSERK binary vector is used to generate the following promoter-AtSERK constructs.

- The AtLTP1 promoter is cloned in the SmaI site of the pAtSERK binary vector as a Klenow-filled *KpnI*-*SstI* DNA fragment to give the pAtLTP1AtSERK vector.
- The CaMV 35S promoter is cloned in the SmaI site of the pAtSERK binary vector as a Klenow-filled *KpnI*-*SstI* fragment to give the p35SAAtSERK vector.
- The AtDMC1 promoter consisting of the *BglII* - *XhoI* 3.3kB fragment from the clone SLJ 9691 is filled in with Klenow and cloned into the SmaI site of the pAtSERK binary vector to give the pAtDMC1AtSERK vector.
- A *SacI*-*KpnI* fragment of FBP2101 is filled in with Klenow and cloned into the SmaI site of the pAtSERK binary vector to give the pFBP2101AtSERK vector.

#### Introduction of plant expression vectors into *Arabidopsis thaliana* plant cells

The above described vector constructs (pAtLTP1AtSERK, p35SAAtSERK, pAtDMC1AtSERK, pFBP2101AtSERK) have been electrotransformed into *Agrobacterium tumefaciens* strain C58C1 as known in the art.

Wild type *Arabidopsis thaliana* WS plants are grown under standard long day conditions: 16 hours light and 8 hours dark.

The first emerging inflorescence is removed in order to increase the

number of inflorescences. Five days later, plants are ready for vacuum infiltration.

*Agrobacterium* strain C58C1 containing the transformation plasmid (the pAtLTP1AtSERK vector or the p35SAAtSERK or the pAtDMC1AtSERK vector or the pFBP2101AtSERK vector) is grown on a LB plate with 50 mg/l kanamycin, 50 mg/l rifampicin and 25 mg/l gentamycin. A single colony is used to inoculate 500 ml of LB medium containing 50 mg/l kanamycin, 50 mg/l rifampicin and 25 mg/l gentamycin. The cultures are grown O/N at 28 degrees Celsius and the resulting log phase culture (OD<sub>600</sub> 0.8) is centrifuged to pellet the cells and resuspended in 150 ml of infiltration medium (0.5x MS medium (pH 5.7) with 5% sucrose and 1 mg/l benzylaminopurine). The inflorescences of 6 *Arabidopsis* plants are submerged in the infiltration suspension while the remaining parts of the plants (which are still potted) are placed upside down on meshed wire to avoid contact with the infiltration suspension.

Vacuum is applied to the whole set-up for 10 min. at 50 kPa. Plants are directly afterwards placed under standard long day conditions. After completed seed setting the seeds are surface sterilized by a 1% sodium hypochlorite soak, then thoroughly rinsed with sterile water and plated onto petridishes with 0.5xMS medium and 80 mg/l kanamycin in order to select for transformed seeds. After 5 days germination under long day conditions (10.000 lux), the transformed seedlings could be identified by their green colour of their cotyledons (the untransformed seedlings turn yellow), and are further grown in soil under long day conditions. This vacuum infiltration method resulted in approximately 0.1% transformed seeds.

#### Expression of SERK sequences in *Arabidopsis thaliana* plant cells

The inflorescences from transgenic and not transgenic *Arabidopsis thaliana* plants are analysed by Whole mount *in situ* hybridisation analysis with AtSERK cDNA as probe. The inflorescences in different stages of development are fixed for 60 min. in PBS containing 70 mM EGTA, 4% paraformaldehyde, 0.25% glutaraldehyde, 0.1% Tween 20, and 10% DMSO. Samples are then washed, treated with proteinase K for 10 min, again washed and fixed a second time. Hybridisation solution consisted of PBS containing 0.1% Tween 20, 330 mM NaCl, 50 mg/ml heparin, and 50% deionized formamide. Hybridisation took place for 16 hours at 42°C using digoxigenin-labeled sense or antisense riboprobes (Boehringer Mannheim). After washing, the cells are treated with RNaseA and incubated with anti-digoxigenin-alkaline phosphatase conjugate (Boehringer Mannheim) which had been preabsorbed with a plant protein extract. Excess antibody is removed by washing followed by rinsing in staining buffer (100 mM Tris-HCl pH 9.5, 100 mM NaCl, 5 mM MgCl<sub>2</sub>, 1 mM levamisole) and the staining reaction is performed for 16 hours in a buffer containing NBT and BCIP. Observations are performed using a Nikon Optiphot microscope equipped with Nomarski optics.

The transformed plants show ectopic expression of SERK in the vicinity of the embryo sac.

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

## (i) APPLICANT:

- (A) NAME: NOVARTIS AG
- (B) STREET: Schwarzwaldallee 215
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- (I) TELEX: 962 991

(ii) TITLE OF INVENTION: Improvements in or relating to organic compounds

(iii) NUMBER OF SEQUENCES: 33

## (iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

## (2) INFORMATION FOR SEQ ID NO: 1:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6695 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown



(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Daucus carota*

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 3696..6617

(ix) FEATURE:

(A) NAME/KEY: intron

(B) LOCATION: 3731..3802

(ix) FEATURE:

(A) NAME/KEY: intron

(B) LOCATION: 3851..3979

(ix) FEATURE:

(A) NAME/KEY: intron

(B) LOCATION: 4124..4211

(ix) FEATURE:

(A) NAME/KEY: intron

(B) LOCATION: 4284..4357

(ix) FEATURE:

(A) NAME/KEY: intron

(B) LOCATION: 4430..4528

(ix) FEATURE:

(A) NAME/KEY: intron

(B) LOCATION: 4642..4757

## (ix) FEATURE:

- (A) NAME/KEY: intron  
(B) LOCATION: 4890..4967

## (ix) FEATURE:

- (A) NAME/KEY: intron  
(B) LOCATION: 5295..5803

## (ix) FEATURE:

- (A) NAME/KEY: intron  
(B) LOCATION: 6197..6339

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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TCTAGATGAC GAAATCGGCG TACCTTTGAT TTNGAAATAC TAGGTTGTAG TATCTTGATT      60
AGTTTTTTGG ATATCTTGCT GTAATTTCCT TAGGAGATGC AAACGGTCTT CATTTAATAT      120
GAGCCCTTGT GACTTGACAA AAGTATCTAG CATGTTTGAT CACGAGGTAG CTAAAAAGTA      180
GGGTGTTTGA TTAAGCACAT AATATTGTAT TGGGCTATT GGCTATCAAT GAAGTTTGAT      240
GCAAGTATAT AGCTTGTAAT ATGCATGTGA TGAGGTATA TAAAGAAGT AAAGAACATT      300
CTCTCGTAGC ATTCATTTTT CTCTGGCTA TAGTTAACGA GTTTTGTAC ACATGACGTT      360
GAAACTGGAT GTGCTGTTT TCCATCTAA GTTTGGATTA CCTGATAGAT GCTCAACTTC      420
TTCTGACGCC TTTCTTTTCC GATTTTCCG AAGACAAGAT TCTTTAGTTA ATAGTTATTG      480
CTCTGGTGGC TTGTGTGCAT TTAGGAATC TTACTCTGTT TTTAATGGA GAAACGAAAC      540
CTACCTTTTT TTCTGTGTT CCTTTTATGA TATCACTGC TTGGAGGGT TTAGACTTTA      600
TCCACCTAAA CTATTCATGT TTACCAGACA AGCTATACGT TTTATCCCC CCCCCGGGG      660
ACCTGNGGAC AAAAGAAGCG CTGATGAAT GATTTAATCC GTGTTTATT ATATTACACA      720

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TTGATGCTTC ATGGAGCTAA TATCTTTGGT TAAATTTTCAT GTATATATAT ACCCTTCCCT 780

CTTGTGATGG CAGTGGCCCC TCGTTTAATT AGCGTACTTA ATTATCTGAT GGATACTGTA 840

TGCTTGGCAG ATGATGTCAT CAGATTATAC CATTGTGTGT GCTCTACAAA ATAAAAAACC 900

TCTATTTATG TTCATCTTTT TGGTAACAAG TAACTAATTG ATGCGCTATG TTGACAGGG 960

ATGCATTACA CAACTTACGA ACTAGCTTGC AAGATCCCAA CAATGTCTG CAGAGCTGGG 1020

ATCCAACCCCT TGTGAACCCCT TGCACATGGT TTCATGTGAC ATGTAACAAT GAAAACAGTG 1080

TTATAAGAGT GTAGGTCAC TCCCTTATTA ATTTTTTTAG CAAGTTACGA ATATTTACTC 1140

AATTGAGCAG ATGTCTCTTT AAATATTTTT CTTTAATTTT TTAGCTAAGC GGAGCATCTA 1200

TCTTAAGTAT CTCTACTGAA TTTAAGACAT AATACATTTT TTTAAAAAT CTATTAGAGT 1260

GTTTTTTCCG CACAGGCGAC ATATATCTTT TTTCTGGTAA TTCAGACAAC CTTTCTCCCG 1320

ACGATAAAAT AATATAAGAT TAACTCCTTG AACTAATTTT TTATTTTTCT TTTCTTTTTA 1380

TGTTCTTTGC AGAAAGTTT TTATGGTCTT TTGTGAAAAG TACATTCTAT GATAATTTTT 1440

TGGCAACTCA TATAAATTTA TATATATTC ATGTAGTTAT AAGTTAAAAA AAGCTTCCTA 1500

TTAATTCCAA GATAGAGGTT CATTTTATA GTTGGGCAT CCATGAGTTT TTGAAAATGT 1560

CAGAAATTTT GTTGAGTTAA TTTTACTTAC CAACTTTTAT GGCGTCATGC AGTGATCTTG 1620

GGAATGCAGC ATTATCTGGT CAATTGGTTC CTCTTGGCCA GTTGAAAAAT TTACAATACT 1680

TGTAAGACCA TATCACTTGG AATGCTTTAG TTTTATACA GCACAATGCT TTCAATATCT 1740

GTTAAAGTG TGAAAAGTT GACTTTCTAG CTTCAGCAGT TGTTCGGATA ATATCTATGA 1800

AGCACTTAAA AGGCTGGGCA ATTTTTTTGT TATTATTTC AATATTGTTA ATTGTTACTA 1860  
 CTTAATATGA TAAACTGATT TAACTCCTCA TGATTGGTCT CAGTCCAATG TGCCCTCAIT 1920  
 AGTCACATNA TAAAAATTGNN GGGTTGGACA AATATAACTT CTTTCTTAA GGTCCAGAAA 1980  
 GAGCACTTAT CAACCTTGTC TAGCGCATAA CGTCACAGTG GGTCACTCAC GGGCTATCCA 2040  
 GTTTGGGGAG GTTTTAATGA GCACCTATTT ACCTTGCTTT TTAACGTCT GAGGATGTTA 2100  
 TTAAAGTCTG CATCATTCAG AGTTTAAAT AGCACTTTCA GTTGATTAT GAATGGTACA 2160  
 TGAAAGATAC ATATCTTAAT GTTCTATGC CTGTTTCAAC ATGCTCTAA TATTCTGTTA 2220  
 TCTTTGTCAT CTTAAAAATG GCACTGATTA AAATGTGAGA AAGGTAGTCT TCCAATACCA 2280  
 TTTCATGTAT ACCAGAGAAT ATCATAATTT TTTTAAATCA TAAGTTGGGC CCTAGAGTTT 2340  
 TCTCAGTATT GGTCTATTTA TATTTTCCAC CATTTAGAAC TGTGTGTCA GATGAAAATC 2400  
 TTGGACTTCC ACAGAAGATC TTATAGTAAA AGTATTCTTT AGATCTGATG ATGAAAGTTG 2460  
 TCATGGTGTG GCGTGCCCA GAATTAAAT CAATCCCATG TCACATGTTT GTTGATCTGA 2520  
 CTACTCACTG TTAATCGAAG AGTAACTATT TGTGAATTAA ATGCTTTTTT TTTTGTCTTT 2580  
 CATGCTTAGC GTTATAAAGG TCTACGCTG ACTATGGTTT TTAACATGTT ATAGTTTTGT 2640  
 ACTGACAAGT TTAAAGTTTC TCTTGTTTAC GAATTAAGAA TATATAATAT AAAACGCTTT 2700  
 AACTTTCTCT GTGGAAGGTG TTCTTACCTT TTTATATATA TATATAGATA CTCAGACTCT 2760  
 GCTGGCAATT ATATCTTACG AACTTACGAG TATACAGAAC TTGTATATTA GGTTCCAGATG 2820  
 AGTGGCTGTA GTAGAACACC TTAAGCAAGA ACTTAATCAT GAGGTTTCAA CCTTTTAACT 2880  
 TTCTTTTTAG ATTTTTTCAA GTTTATGGAA AATTGTACCT CATGATCGTG GTTCTTTCC 2940

ATAAACTTTC CATATAAGTC CGTTTCTTGA CGTTTTTCATG TAAGCTGTTG ACGAGTGATT 3000  
 ATTAGCGGTT CTTTCAATAA TCATAATGTG TCTCACTTTG ATGAGGCCTG TACTTATTAT 3060  
 TGCACCTTGC ACTTAACCTT GATCCTCATG TCATCTTGAT TGTCAATAGTC TACTAACCGA 3120  
 GTTGAACATG GTTTATCATG TCTTTTGAGG TAACAATGTA GCTTTCACCT CTGTCTTGA 3180  
 TATAGGTTTA AGGCTTGCAC CTCCCACTAG CCTTCGTTG TTTTATTAC AGTTCACACA 3240  
 CCTACTAGCA CTGTTCACCT CTAGTCTTTT GTCGCAAAAT AGTAAGAAGT TTCTTTGCA 3300  
 TAATAGTGGT TGATCATTTA AGAAATAGTG AATCAAATTA TCGTGTTATT GTGTTGTAC 3360  
 TTTGGAATTA AATGAGTTGC TGAACATTGT TGCTGTTTAT CGTTGTCAAG GCTTTGCCAA 3420  
 GGAAGGCGAT TAGTAAGAGT GGGCATCCAA GCGCCTTTAT CTGAAGGGG CGGGCGGCAC 3480  
 GTTGIGGATT CTGGGIGTCT ATTAGAGGAC ATTATCTATA TATACTGATT ATTTATTAGA 3540  
 ATATAAATCA ACTACTATAT TTTTCTTTGT AATGTTTATA TAGAAATCCC ACTCGTAAAC 3600  
 TTGACAAATA CCATTGAAAT ATTTGAACCT AATTAAATTAG TAGTGTCAAG TTTAAATTCA 3660  
 AACTCATTTA ATTTTACTTT AAAAAATAAT TCTATATGAA TCGTAACAGT ATAAATATAT 3720  
 TAAATTACAT GTATGTGTGC CTATATATAG CTGAATGTCT AATAGACTCC AAGACGGCTG 3780  
 CTCCTACTGC CTAGGCTCC AGGCAGTTCA CTGATGCTTA CCTTGACAAA TATGGGGTTC 3840  
 GTATGACATT GTTGGGGATC CCTATCACTG GATTCCGTGT TTGCTGACCC TCTGTCAAT 3900  
 TGATTTTCAT TGATGTAGTA TTACTAGTTT TATAAATATT CTTTATGCA ATAATTTAAC 3960  
 TGGAGTTTAA CAATGACAGG GAGCTTTCAC GCAATAACAT AAGTGGACCA ATTCTAGTG 4020

ATCTTGGGAA TCTGACAAAT TTGGTGAGCT TGGACCTATA CATGAATAGC TTCTCTGGAC 4080  
 CTATACCGGA CACATTAGGA AAGCTTACAA GGCTAAGATT CTTGTATGAC TACAAATCTT 4140  
 CACTAGTTTT TAACTTAATG CAATTGATT ATCCTTTCAA GTGATTGATT ATATCACAAA 4200  
 TTA CTGGATA GCGCTCTCAA CAACAAC TGC CTCTCTGGTC CAATTOCAAT GTCAC TGA CT 4260  
 AATATTACAA CTCTTCAAGT CCTGTAAGTA TTCCGACCTT TCCAGATAGT TTTGTGTGTG 4320  
 TGGATGTTTC AATTTAATA CTAAATATGT TCATCAGGGA TTTATCAAAC AATCGGCTAT 4380  
 CAGGACCACT ACCGATAAT GGCTCATTTT CTTTGTMTAC ACCTATCAGG TTTAATGCTA 4440  
 GTAATATCTT TAATATTATG GTTCTTACTT CTA CTGCGAA AGCTATGATA ATATTTTTTT 4500  
 TCTCCTTCAT ATATTATCAC TTTCGCAGTT TTGGCAATAA TTTGAATTTA TGTGGACCTG 4560  
 TAACTGGGAG GCCCTGCCCT GGATCTCCCC CATTTTCTCC ACCACCTCCG TTCATCCAC 4620  
 CATCAACAGT ACAGCTCCA GGTGATTTAG TTTTATATT AATCCCGTA ATTAATTTTA 4680  
 TGA CTG TAAA AATTGGTGT AATTTCACCA GTTGC GAATA AAGTATTTTC CTTCTTCTC 4740  
 TTCTTATTAT TATGAAGGAC AAAATGGTCC CACTGGAGCT ATTGCTGGG GAGTAGCTGC 4800  
 TGGTGCTGCT TTA CTGTTTG CTGCACTGC AATGGCATTT GCATGGTGGC GGAGAAGAAA 4860  
 ACCGOGAGAA CATTTCTTTG ATGTGCCAGG TTAGTCTGT AAATAGATAT CTATTGAAGC 4920  
 GCTTACTGTC TGTGGACTTT GTTTTCACTG TCATTAGTTA ACTTCAGCTG AAGAGGACCT 4980  
 AGAAGTGCAC CTTGGTCAAC TGAAGAGGTT TTCTCTGCGA GAATTGCAAG TCGCAACGGA 5040  
 TACTTTTAGT ACCATCTTG GAAGAGGTG ATTTGGTAAG GTGTATAAGG GACGCCTTGC 5100  
 TGATGGCTCA CTTGTAGCAG TTAAAAGGCT TAAAGAAGAA CGAACACCAG GTGGCGAGCT 5160

GCAGTTTCAA ACAGAAGTGG AAATGATTAG CATGGCTGTG CATCGAAATC TTCTGCGTCT 5220

ACGTGGTTTC TGCATGACAC CTACCGAGCG GCTTCTTGTA TATCCATACA TGGCTAATGG 5280

AAGTGTTCGG TCATGTTTAA GAGGTATCTC AGTTACAATT ACCATAACTT GCCAGAAGTT 5340

TGTTTGATTA AAAATGAAAT ATAACTCCCT ACACTATGTT AAGGTGTTAT AATTTCGAG 5400

CAGATCTTAT TTCCATTGC AAGATACCAG TTATTATTGT TTTTCTGTA ATTGATACCG 5460

GTTATATTTC TTTCTTGAT TTGTTTATAT GCAAGGATTT CGAGTCTAAT AAGTTATCAA 5520

ACTGGATGCT ATGTTTATTC TGCAATTGAA TTCTTGCTTC ATGTGCCAAA ATATATATGA 5580

TTCAACTTGG AATCATCTTA TAATATACTG TGTAAAGTCA GCTGTGACT TTCATCATTA 5640

ATTAGTCTTC ATAAATCAGA ATCTGCCTAG TGAGCTTTAC CGACATACTC TAAACCTTTC 5700

TTATGGCCCT GTATATAATC GTCCACTTA CTTTATTCAG TTTGTCTGCT CTCGAATTT 5760

TTGATCTGTA CATGTGATG TCTTGTTTTT ATCAAATGTA GAGCGTCAGC CATCAGAACC 5820

TCCCCCTGAT TGGCCAATA GGGAGAGGAT TGCCTAGGA TCTCTAGGG GCGTATCTAA 5880

ATTGCATGAC CATGTGATC CCAAGATTAT CCATCGCGAT GTAAAAGCTG CAAATATATT 5940

ATTGGACGAA GAATTGAGG CTGTGTAGG TGATTTTGGG TTAGCTAGGC TCATGGATTA 6000

CAAGGATACC CATGTTACGA CTGCTGTAAG GGGTACCATT GGGCACATAG CTCCCGAGTA 6060

CCTCTCGACT GGAAAGTCAT CAGAGAAGAC CGATGCTTTT GGTATGGGA TAATGCTCCT 6120

AGAGCTCATT ACTGGACAGA GGGCTTTTGA TCTTGCTCGC CTTGCGAACC ATGATGATGT 6180

TAIGTTGTTC GATTGGGTAT GTGTCCCGG TGTTCCTTTG GTTAATTATT TCACATATTA 6240

GIGCTTACTA CTTTGTGTG GGCCTTTGTT TTTATTTCTT GCTGTATTT GATTCTTAGT 6300  
CATGTTATGC ATATTGACCT GCCTTGCAAT GTCTTTTAGG TTAAAAGCCT TTGAAAGAG 6360  
AAAAAGTTGG AGATGCTGGT CGATCCTGAC CTGCAGAACA ATTACATTGA CACAGAAGTT 6420  
GAGCAGCTTA TTCAAGTAGC ATTACTCTGT ACCCAGGGTT CGCCAATGGA GCGGCCTAAG 6480  
ATGTCAGAGG TAGTCCGAAT GCTTGAAGGT GATGGCCTTG CAGAAAAGTG GGACGAGTGG 6540  
CAAAAAGTTG AAGTCATCCA TCAAGACGTA GAATTAGCTC CACATCGAAC TTCTGAATGG 6600  
ATCCTAGACT CGACAGATAA CTTGCATGCT TTTGAATTAT CTGGTCCAAG ATAAACAGCA 6660  
TATAAAATGT AATGAAATTA ATATTTTTTA TGGTT 6695

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1815 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Daucus carota*

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 94..1752



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

GACAAATACC ATTGAAATAT TTGAACCTAA TTAATTAGTA GTGTCAGGTT TAAATTCAAA	60
CTCATTTAAT TTTACTTTAA AAAATAATTC TAT ATG AAT CGT AAC AGT ATA AAT	114
Met Asn Arg Asn Ser Ile Asn	
1 5	
ATA TTA AAT TAC ATG CAG TTC ACT GAT GCT TAC CTT GAC AAA TAT GGG	162
Ile Leu Asn Tyr Met Gln Phe Thr Asp Ala Tyr Leu Asp Lys Tyr Gly	
10 15 20	
GTT CTT ATG ACA TTG GAG CTT TAC AGC AAT AAC ATA AGT GGA CCA ATT	210
Val Leu Met Thr Leu Glu Leu Tyr Ser Asn Asn Ile Ser Gly Pro Ile	
25 30 35	
CCT AGT GAT CTT GGG AAT CTG ACA AAT TTG GTG AGC TTG GAC CTA TAC	258
Pro Ser Asp Leu Gly Asn Leu Thr Asn Leu Val Ser Leu Asp Leu Tyr	
40 45 50 55	
ATG AAT AGC TTC TCT GGA CCT ATA CCG GAC ACA TTA GGA AAG CTT ACA	306
Met Asn Ser Phe Ser Gly Pro Ile Pro Asp Thr Leu Gly Lys Leu Thr	
60 65 70	
AGG CTA AGA TTC TTG CGT CTC AAC AAC AAC AGC CTC TCT GGT CCA ATT	354
Arg Leu Arg Phe Leu Arg Leu Asn Asn Asn Ser Leu Ser Gly Pro Ile	
75 80 85	
CCA ATG TCA CTG ACT AAT ATT ACA ACT CTT CAA GTC CTG GAT TTA TCA	402
Pro Met Ser Leu Thr Asn Ile Thr Thr Leu Gln Val Leu Asp Leu Ser	
90 95 100	
AAC AAT CGG CTA TCA GGA CCA GTA CCG GAT AAT GGC TCA TTT TCT TTG	450
Asn Asn Arg Leu Ser Gly Pro Val Pro Asp Asn Gly Ser Phe Ser Leu	
105 110 115	
TTT ACA CCT ATC AGT TTT GCC AAT AAT TTG AAT TTA TGT GGA CCC GTA	498



265	270	275	
AGC ATG GCT GTG CAT CGA AAT CTT CTG CGT CTA CGT GGT TTC TGC ATG			978
Ser Met Ala Val His Arg Asn Leu Leu Arg Leu Arg Gly Phe Cys Met			
280	285	290	295
ACA CCA ACA GAG CCG CTT CTT GTA TAT CCA TAC ATG GCT AAT GGA AGT			1026
Thr Pro Thr Glu Arg Leu Leu Val Tyr Pro Tyr Met Ala Asn Gly Ser			
300	305	310	
GTT GCG TCG TGT TTA AGA GAG CGT CAG CCA TCA GAA CCT CCC CTT GAT			1074
Val Ala Ser Cys Leu Arg Glu Arg Gln Pro Ser Glu Pro Pro Leu Asp			
315	320	325	
TGG CCA ACT AGG AAG AGG ATT GCA CTA GGA TCT GCT AGG GGG CTT TCT			1122
Trp Pro Thr Arg Lys Arg Ile Ala Leu Gly Ser Ala Arg Gly Leu Ser			
330	335	340	
TAT TTG CAT GAC CAT TGT GAT CCC AAG ATT ATC CAT CGT GAT GTA AAA			1170
Tyr Leu His Asp His Cys Asp Pro Lys Ile Ile His Arg Asp Val Lys			
345	350	355	
GCT GCA AAT ATA TTA TTG GAC GAA GAA TTT GAG GCT GTT GTA GGT GAT			1218
Ala Ala Asn Ile Leu Leu Asp Glu Glu Phe Glu Ala Val Val Gly Asp			
360	365	370	375
TTT GGG TTA GCT AGG CTC ATG GAT TAC AAG GAT ACC CAT GTT ACA ACT			1266
Phe Gly Leu Ala Arg Leu Met Asp Tyr Lys Asp Thr His Val Thr Thr			
380	385	390	
GCT GTA AGG GGT ACC TTG GGC TAC ATA GCT CCC GAG TAC CTC TCG ACT			1314
Ala Val Arg Gly Thr Leu Gly Tyr Ile Ala Pro Glu Tyr Leu Ser Thr			
395	400	405	
GGA AAG TCA TCA GAG AAG ACC GAT GTC TTT GGT TAT GGG ATT ATG CTC			1362
Gly Lys Ser Ser Glu Lys Thr Asp Val Phe Gly Tyr Gly Ile Met Leu			
410	415	420	

TTA GAG CTC ATT ACT GGA CAG AGA GCT TTT GAT CTT GCT CGC CTT GCG	1410
Leu Glu Leu Ile Thr Gly Gln Arg Ala Phe Asp Leu Ala Arg Leu Ala	
425 430 435	
AAC GAT GAT GAT GTT ATG TTG TTG GAT TGG GTT AAA AGC CTT TTG AAA	1458
Asn Asp Asp Asp Val Met Leu Leu Asp Trp Val Lys Ser Leu Leu Lys	
440 445 450 455	
GAG AAA AAG TTG GAG ATG CTG GTC GAT CCT GAC CTG GAG AAC AAT TAC	1506
Glu Lys Lys Leu Glu Met Leu Val Asp Pro Asp Leu Glu Asn Asn Tyr	
460 465 470	
ATT GAC ACA GAA GTT GAG CAG CTT ATT CAA GTA GCA TTA CTC TGT ACC	1554
Ile Asp Thr Glu Val Glu Gln Leu Ile Gln Val Ala Leu Leu Cys Thr	
475 480 485	
CAG GGT TCG CCA ATG GAG CGG CCT AAG ATG TCA GAG GTA GTC CGA ATG	1602
Gln Gly Ser Pro Met Glu Arg Pro Lys Met Ser Glu Val Val Arg Met	
490 495 500	
CTT GAA GGT GAT GGC CTT GCA GAA AAG TGG GAC GAG TGG CAA AAA GTA	1650
Leu Glu Gly Asp Gly Leu Ala Glu Lys Trp Asp Glu Trp Gln Lys Val	
505 510 515	
GAA GTC ATC CAT CAA GAC GTA GAA TTA GCT CCA CAT CGA ACT TCT GAA	1698
Glu Val Ile His Gln Asp Val Glu Leu Ala Pro His Arg Thr Ser Glu	
520 525 530 535	
TGG ATC CTA GAC TCG ACA GAT AAC TTG CAT GCT TTT GAA TTA TCT GGT	1746
Trp Ile Leu Asp Ser Thr Asp Asn Leu His Ala Phe Glu Leu Ser Gly	
540 545 550	
CCA AGA TAAACAGCAT ATAAATGTG AATGAAATTA ATATTTTTTA TGGTTAAAAA	1802
Pro Arg	

AAAAAAAAAA AAA

1815

## (2) INFORMATION FOR SEQ ID NO: 3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 553 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Met	Asn	Arg	Asn	Ser	Ile	Asn	Ile	Leu	Asn	Tyr	Met	Gln	Phe	Thr	Asp
1				5					10					15	
Ala	Tyr	Leu	Asp	Lys	Tyr	Gly	Val	Leu	Met	Thr	Leu	Glu	Leu	Tyr	Ser
			20					25					30		
Asn	Asn	Ile	Ser	Gly	Pro	Ile	Pro	Ser	Asp	Leu	Gly	Asn	Leu	Thr	Asn
		35				40						45			
Leu	Val	Ser	Leu	Asp	Leu	Tyr	Met	Asn	Ser	Phe	Ser	Gly	Pro	Ile	Pro
	50					55						60			
Asp	Thr	Leu	Gly	Lys	Leu	Thr	Arg	Leu	Arg	Phe	Leu	Arg	Leu	Asn	Asn
65				70				75						80	
Asn	Ser	Leu	Ser	Gly	Pro	Ile	Pro	Met	Ser	Leu	Thr	Asn	Ile	Thr	Thr
			85					90					95		
Leu	Gln	Val	Leu	Asp	Leu	Ser	Asn	Asn	Arg	Leu	Ser	Gly	Pro	Val	Pro
		100						105					110		
Asp	Asn	Gly	Ser	Phe	Ser	Leu	Phe	Thr	Pro	Ile	Ser	Phe	Ala	Asn	Asn
		115						120					125		

Leu Asn Leu Cys Gly Pro Val Thr Gly Arg Pro Cys Pro Gly Ser Pro  
 130 135 140

Pro Phe Ser Pro Pro Pro Phe Ile Pro Pro Ser Thr Val Gln Pro  
 145 150 155 160

Pro Gly Gln Asn Gly Pro Thr Gly Ala Ile Ala Gly Gly Val Ala Ala  
 165 170 175

Gly Ala Ala Leu Leu Phe Ala Ala Pro Ala Met Ala Phe Ala Trp Trp  
 180 185 190

Arg Arg Arg Lys Pro Arg Glu His Phe Phe Asp Val Pro Ala Glu Glu  
 195 200 205

Asp Pro Glu Val His Leu Gly Gln Leu Lys Arg Phe Ser Leu Arg Glu  
 210 215 220

Leu Gln Val Ala Thr Asp Thr Phe Ser Thr Ile Leu Gly Arg Gly Gly  
 225 230 235 240

Phe Gly Lys Val Tyr Lys Gly Arg Leu Ala Asp Gly Ser Leu Val Ala  
 245 250 255

Val Lys Arg Leu Lys Glu Glu Arg Thr Pro Gly Gly Glu Leu Gln Phe  
 260 265 270

Gln Thr Glu Val Glu Met Ile Ser Met Ala Val His Arg Asn Leu Leu  
 275 280 285

Arg Leu Arg Gly Phe Cys Met Thr Pro Thr Glu Arg Leu Leu Val Tyr  
 290 295 300

Pro Tyr Met Ala Asn Gly Ser Val Ala Ser Cys Leu Arg Glu Arg Gln  
 305 310 315 320

Pro Ser Glu Pro Pro Leu Asp Trp Pro Thr Arg Lys Arg Ile Ala Leu

325	330	335	
Gly Ser Ala Arg Gly Leu Ser Tyr Leu His Asp His Cys Asp Pro Lys			
340	345	350	
Ile Ile His Arg Asp Val Lys Ala Ala Asn Ile Leu Leu Asp Glu Glu			
355	360	365	
Phe Glu Ala Val Val Gly Asp Phe Gly Leu Ala Arg Leu Met Asp Tyr			
370	375	380	
Lys Asp Thr His Val Thr Thr Ala Val Arg Gly Thr Leu Gly Tyr Ile			
385	390	395	400
Ala Pro Glu Tyr Leu Ser Thr Gly Lys Ser Ser Glu Lys Thr Asp Val			
405	410	415	
Phe Gly Tyr Gly Ile Met Leu Leu Glu Leu Ile Thr Gly Gln Arg Ala			
420	425	430	
Phe Asp Leu Ala Arg Leu Ala Asn Asp Asp Asp Val Met Leu Leu Asp			
435	440	445	
Trp Val Lys Ser Leu Leu Lys Glu Lys Lys Leu Glu Met Leu Val Asp			
450	455	460	
Pro Asp Leu Glu Asn Asn Tyr Ile Asp Thr Glu Val Glu Gln Leu Ile			
465	470	475	480
Gln Val Ala Leu Leu Cys Thr Gln Gly Ser Pro Met Glu Arg Pro Lys			
485	490	495	
Met Ser Glu Val Val Arg Met Leu Glu Gly Asp Gly Leu Ala Glu Lys			
500	505	510	
Trp Asp Glu Trp Gln Lys Val Glu Val Ile His Gln Asp Val Glu Leu			
515	520	525	

Ala Pro His Arg Thr Ser Glu Trp Ile Leu Asp Ser Thr Asp Asn Leu  
530 535 540

His Ala Phe Glu Leu Ser Gly Pro Arg  
545 550

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

TTTTTTTTTT TGC

13

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO



(vi) ORIGINAL SOURCE:

(A) ORGANISM: primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

GGGATCTAAG

10

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

ACACGTGGTC

10

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

TCAGCACAGG

10

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

TTTTTTTTTT TCTG

14

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

TTTTTTTTTT TCA

13

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

GACATCGTCC

10

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

CCCTACTGGT

10

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

ACACGTGGTC

10

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

GGTGACTGTC

10

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

TCTTGACCA GATAATTC

18

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

CTCTGATGAC TTTCAGTC

19

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

AATGGCATTG GCATGG

16

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Daucus carota*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

Ser Pro Pro Pro Pro

1 5

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Daucus carota*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

His Arg Asp Val Lys Ala Ala Asn

1

5

## (2) INFORMATION FOR SEQ ID NO: 19:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Daucus carota

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

Gly Thr Leu Gly Tyr Ile Ala Pro Glu

1

5

## (2) INFORMATION FOR SEQ ID NO: 20:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4081 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

## (vi) ORIGINAL SOURCE:



(A) ORGANISM: *Arabidopsis thaliana*

(vii) IMMEDIATE SOURCE:

(B) CLONE: *Arabidopsis* SERK gene

(ix) FEATURE:

(A) NAME/KEY: exon

(B) LOCATION: 1280..1367

(ix) FEATURE:

(A) NAME/KEY: exon

(B) LOCATION: 1796..1928

(ix) FEATURE:

(A) NAME/KEY: exon

(B) LOCATION: 2014..2085

(ix) FEATURE:

(A) NAME/KEY: exon

(B) LOCATION: 2203..2346

(ix) FEATURE:

(A) NAME/KEY: exon

(B) LOCATION: 2450..2521

(ix) FEATURE:

(A) NAME/KEY: exon

(B) LOCATION: 2617..2688

(ix) FEATURE:

(A) NAME/KEY: exon

(B) LOCATION: 2772..2884

(ix) FEATURE:

(A) NAME/KEY: exon

(B) LOCATION: 3015..3146

## (ix) FEATURE:

(A) NAME/KEY: exon

(B) LOCATION: 3305..3646

## (ix) FEATURE:

(A) NAME/KEY: exon

(B) LOCATION: 3760..4081

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

TCTAGAAACC TTTTGATCAT AATGAAAATA AAGAGTCCAT CCACCACATG GGGTAAGCAT	60
AATGTGTGAT ATTAAAGGG TAACAAATGT AATCTGCTTT TTATTTTACT TTTTACCTCT	120
ACTCAAATG TATGGGCAGT TTTTTTTTTT TTTTAAATGA TAAGACAAGT ATCTGTTTAA	180
TGGTATTGTG ATGAAACAGT AGTAAAGTCA TATCGGGCAC GCCATACTAC TTCCACAGTG	240
GAACTTGGCC AAATTTTGTG TTGCGGTCT CTACAGTTTC TTCCACCAA TTTTTGTTG	300
ACAAACTCA AATCTTTCAA TCTCATCTCT GCCAAAGTGG GGTTAGAAA GAATATCAGC	360
AAACACTAAT ATCTTTATG TTGCATGGTT TATCAATCAC AAAATTCACA ACCATTGTAA	420
AAAAAAATTC ACATTTTGG TATGAGATTG CTCACATGAT AGTGAACCTC TTTAACATTT	480
TAACTTTACT TTCATAAATA CGGATTACG AATCTTACTT GCATTAAAA TTTAGAAAAG	540
GTTTTCTAC TTAAAGAAAA AAGGGACCCA ACAGAGAGAG GTTTGACCAG GAGAAACGGG	600
TGCATAGCCT TAAGAGCTTT CAACTACTTT ACCCCAAACC CAAAGCGATG TCACTTTCAA	660
CCATCTCTTC TCTCCCCGA ACCCGTTTTT TTGACCGGTC AGTTCGGGCA GCAGCACCGT	720
TACGGGCAGC TTATATTCTT CGTCTCTCTC CTCTACACCA CTGCATGCC ATAAATAAAG	780

CCCGTGGAGA TCTTTAAAAA TATTAAATAA TATATCAACG AAAAAGCTAT TTTATTCATA	840
AGAAGAAAAA GAGAGGAACA ACAACAACAC ACTAATCATA GTTCTCTGG CAGGCTTGT	900
GTTCGGCTT AATAAAAAGC TCTTTTGTTA TTATTACTTC ACGTAGATTT TCCCCAAAAA	960
GCTCTTATTT TTTTGTTTAA AAAAAAAGT TTCATCTTTA TTCAACTTTT GTTTTACAGT	1020
GTGTGTGTGA GAGAGAGAGT GTGGTTTGAT TGAGGAAAGA CGACGACGAG AACGCCGAG	1080
AATTAGGATT TTTATTTTAT TTTTACTCT TTGTTTGTT TAATGCTAAT GGGTTTTTAA	1140
AAGGGTTATC GAAAAAATGA GTGAGTTTGT GTTGAGGTG TCTCTGTAA GTGTTAATGG	1200
TGGTATTTT CGGAAGTTAG GGTTCCTCG GATCTGAAGA GATCAAATCA AGATTGAAA	1260
TTTAGCATG TTGTTTAAA TGGAGTCGAG TTATGTGGTG TTTATCTTAC TTCACTGAT	1320
CTTACTTCG AATCATTCAC TGTGGCTTGC TTCTGCTAAT TTGGAAGGTT CGTGGTACT	1380
CAATTACTCA GCTTACTCG TTCTCAATT ACTTCTCGA TTCTTTTTTA TTGGAGGTG	1440
AATCGCTATC TTTAGTGTCT GCATTTTGAT TTATGAAAAT TGTGTTGTT CTGTGATTT	1500
GTAAGATTTA GTGGCTAGTA CTTGAATAC ACTGTTTGC TTTCTTGT CAGATCAACT	1560
TTGTATATTG TAAAGGCATG TTCTTGGGT TGAAAAGCTG GGTATTTGA TATCTTAA	1620
TTGATGTGT TGATCCAAAC ATTCTCTGAA AGACTTCATT TGTTTTGGT TTGTAAAGA	1680
ATTGTTTTAA TTATTAGCT CTAATCTCAG AGAGGCTGT TTGAATAGTT CTCTCTGAA	1740
ATTAGACTTT TCACCAATTG ATGCTAATTG TGTAGATTG TTGTTCTGT TATAGGTGAT	1800
GCTTGCATA CTTGAGGGT TACTCTAGTT GATCCAAACA ATGCTTGCA GAGCTGGGAT	1860
CCTACGCTAG TGAATCCTG CACATGGTTC CATGTCACTT GCAACAACGA GAACAGTGT	1920

ATAAGAGTGT AAAGCTTTCT TCTACTAATC CCACTTTTTA AACTTTGACC TCAGCGTGGT 1980

TACCGACATT TTGTTTTCTT TTGICAAATA CAGTGATTG GGGAAATGCAG AGTTATCTGG 2040

CCATTTAGTT CCAGAGCTTG GTGTGCTCAA GAATTTGCAG TATTGTAAAG TTCCACTTAT 2100

GCATCATGCT TTAACAAAAC AAATCCAAGA TTGACAGAA GAAGCACTGG AGTTACCTTT 2160

TGTAATGAA ATCTTTTAA CAAGTTTCTT ATTTTCTTAC AGGGAGCTTT ACAGTAACAA 2220

CATAACTGGC CCGATTCTTA GTAATCTTGG AAATCTGACA AACTTAGTGA GTTTGGATCT 2280

TTACTTAAAC AGCTTCTCGG GTCCTATTCC GGAATCATTG GGAAAGCTTT CAAAGCTGAG 2340

ATTTCTGIGA GTATACATAT GCTTTACCGG CTCAGTTACA GTCTTTGTTT AATCTTAGGT 2400

TTTGTTCOA TTTTGTACTC TTGTCTGAAA ATTTTACATG CAAGAATAGC CGGCTTAACA 2460

ACAACAGTCT CACTGGGICA ATTCTATGT CACTGACCAA TATTACTACC CTCAAGTGT 2520

TGTGAGTCT CTCATTAACT TTCATTTATG TCTACTTCAT TCTCCCTCAG TTGATTTGTT 2580

GAGTTAATGC ACTTAACCTT GATGGATGCA ACACAGAGAT CTATCAAATA ACAGACTCTC 2640

TGGTTCAGTT CCGACAAATG GCTCCTTCCTC ACTCTTCACA CCCATCAGGT TCTATGATTT 2700

ATCCTCTTCA GTTATTTAG TTGTTGTGTC AGTGCTGAA CTATTCTGA AACTTTCATT 2760

TCCTGTGCA GTTTTGCTAA TAACTTAGAC CTATGTGGAC CTGTACAAG TCACCCATGT 2820

CCTGGATCTC CCGGTTTTT TCTCCACCA CTTTTATTTC AACCTCCCC AGTTCCACC 2880

CCGAGTAAGC CTCTCTTTT TAGTTTACAT TATAGGAAC AGAAGATGAA ATCTTTGCTT 2940

CTCTGCAAT CTTTTTCTC ATATACTCA TCTTGCCAAT AAGGCAATA CCAAATGATC 3000

TAATTTGATT TCAGGTGGGT ATGGTATAAC TGGAGCAATA GCTGGTGGAG TTGCTGCAGG	3060
TGCTGCTTTG CTCTTTGCTG CTCCTGCAAT AGCCTTTGCT TGGTGGCGAC GAAGAAAGCC	3120
ACTAGATATT TTCTTCGATG TGCCTGGTGA GTTTATTATT CGCATTAGTT TCTGTTCTTA	3180
GCCAGCAATT TTGTTTTGCA GAAAAGTATT GGAACAACTG TTAATGAAAA TCAATACATA	3240
AGTCATTGTT TTTTAAGTTA CAAACTCTTT TGAGTAAAAT CTCGATTGCA AAATCTCTAT	3300
GCAGCGAAG AAGATCCAGA AGTTCATCTG GCACAGCTCA AGAGGTTTTC TTGCGGGAG	3360
CTACAAGTGG CGAGTGATGG GTTTAGTAAC AAGAACATTT TGGGCAGAGG TGGGTTTGGG	3420
AAAGTCTACA AGGGACGCTT GGCAGACGGA ACTCTTGTG CTGTCAAGAG ACTGAAGGAA	3480
GAGCGAACTC CAGGTGGAGA GCTCCAGTTT CAAACAGAAG TAGAGATGAT AAGTATGGCA	3540
GTTCATCGAA ACCTGTGAG ATTACGAGGT TTCTGTATGA CACCGACCGA GAGATTGCTT	3600
GTGTATCCTT ACATGGCCAA TGAAGTGTT GCTTCGTGTC TCAGAGGTAA AACTAAACA	3660
ATTAAACATC TTGTGCTCTC TCTCAATTAC TTGACGTGA AGTGTTTTTT CATGTTTTC	3720
TTTATGGGTT CATAATTGTT GGTTACACTA ATGACACAGA GAGGCCACCG TCACAACTC	3780
CGCTTGATTG GCCAAGCGG AAGAGAATCG CGCTAGGCTC AGCTCGAGGT TTGTCTTACC	3840
TACATGATCA CTGCGATCCG AAGATCATT ACCGTGACGT AAAAGCAGCA AACATCCTCT	3900
TAGACGAAGA ATTGGAAGCG GTTGTGGAG ATTTGGGTT GCCAAAGCTA ATGGACTATA	3960
AAGACACTCA CGTGACAACA GCACTCCGTG GCACCATCGG TCACATCGCT CCAGAATATC	4020
TCTCAACCGG AAAATCTTCA GAGAAAACCG ACGTTTTCGG ATACGGAATC ATGCTTCTAG	4080
A	4081

## (2) INFORMATION FOR SEQ ID NO: 21:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 494 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: NO

## (v) FRAGMENT TYPE: N-terminal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

```

Met Glu Ser Ser Tyr Val Val Phe Ile Leu Leu Ser Leu Ile Leu Leu
1           5           10          15

Pro Asn His Ser Leu Trp Leu Ala Ser Ala Asn Leu Glu Gly Asp Ala
          20          25          30

Leu His Thr Leu Arg Val Thr Leu Val Asp Pro Asn Asn Val Leu Gln
          35          40          45

Ser Trp Asp Pro Thr Leu Val Asn Pro Cys Thr Trp Phe His Val Thr
          50          55          60

Cys Asn Asn Glu Asn Ser Val Ile Arg Val Asp Leu Gly Asn Ala Glu
65          70          75          80

Leu Ser Gly His Leu Val Pro Glu Leu Gly Val Leu Lys Asn Leu Gln
          85          90          95

```

Glu Leu Tyr Ser Asn Asn Ile Thr Gly Pro Ile Pro Ser Asn Leu Gly  
 100 105 110

Asn Leu Thr Asn Leu Val Ser Leu Asp Leu Tyr Leu Asn Ser Phe Ser  
 115 120 125

Gly Pro Ile Pro Glu Ser Leu Gly Lys Leu Ser Lys Leu Arg Phe Leu  
 130 135 140

Arg Leu Asn Asn Asn Ser Leu Thr Gly Ser Ile Pro Met Ser Leu Thr  
 145 150 155 160

Asn Ile Thr Thr Leu Gln Val Leu Asp Leu Ser Asn Asn Arg Leu Ser  
 165 170 175

Gly Ser Val Pro Asp Asn Gly Ser Phe Ser Leu Phe Thr Pro Ile Ser  
 180 185 190

Phe Ala Asn Asn Leu Asp Leu Cys Gly Pro Val Thr Ser His Pro Cys  
 195 200 205

Pro Gly Ser Pro Pro Phe Ser Pro Pro Pro Pro Phe Ile Gln Pro Pro  
 210 215 220

Pro Val Ser Thr Pro Ser Gly Tyr Gly Ile Thr Gly Ala Ile Ala Gly  
 225 230 235 240

Gly Val Ala Ala Gly Ala Ala Leu Leu Phe Ala Ala Pro Ala Ile Ala  
 245 250 255

Phe Ala Trp Trp Arg Arg Arg Lys Pro Leu Asp Ile Phe Phe Asp Val  
 260 265 270

Pro Ala Glu Glu Asp Pro Glu Val His Leu Gly Gln Leu Lys Arg Phe  
 275 280 285

Ser Leu Arg Glu Leu Gln Val Ala Ser Asp Gly Phe Ser Asn Lys Asn

290	295	300	
Ile Leu Gly Arg Gly Gly	Phe Gly Lys Val Tyr Lys Gly Arg Leu Ala		
305	310	315	320
Asp Gly Thr Leu Val Ala Val	Lys Arg Leu Lys Glu Glu Arg Thr Pro		
325	330	335	
Gly Gly Glu Leu Gln Phe Gln Thr	Glu Val Glu Met Ile Ser Met Ala		
340	345	350	
Val His Arg Asn Leu Leu Arg Leu Arg Gly Phe Cys Met Thr Pro Thr			
355	360	365	
Glu Arg Leu Leu Val Tyr Pro Tyr Met Ala Asn Gly Ser Val Ala Ser			
370	375	380	
Cys Leu Arg Glu Arg Pro Pro Ser Gln Pro Pro Leu Asp Trp Pro Thr			
385	390	395	400
Arg Lys Arg Ile Ala Leu Gly Ser Ala Arg Gly Leu Ser Tyr Leu His			
405	410	415	
Asp His Cys Asp Pro Lys Ile Ile His Arg Asp Val Lys Ala Ala Asn			
420	425	430	
Ile Leu Leu Asp Glu Glu Phe Glu Ala Val Val Gly Asp Phe Gly Leu			
435	440	445	
Ala Lys Leu Met Asp Tyr Lys Asp Thr His Val Thr Thr Ala Val Arg			
450	455	460	
Gly Thr Ile Gly His Ile Ala Pro Glu Tyr Leu Ser Thr Gly Lys Ser			
465	470	475	480
Ser Glu Lys Thr Asp Val Phe Gly Tyr Gly Ile Met Leu Leu			
485	490		



## (2) INFORMATION FOR SEQ ID NO: 22:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1106 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA to mRNA

## (iii) HYPOTHETICAL: NO

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 142..795

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

TCGACCCACG CGTCGTCOA ACTTCAATAA AGGGGAAACC AACGTAAACC TAATTTTGCT	60
TTCTCCTCTT TGTTTCAGAAA ATTTTCCCTT TACTCTCAAA TTCCCTTTTCG ATTTCCTCT	120
CTTAAACCTC CGAAAGCTCA C ATG GCG TCT CGA AAC TAT CGG TGG GAG CTC	171
Met Ala Ser Arg Asn Tyr Arg Trp Glu Leu	
1 5 10	
TTC GCA GCT TCG TTA ACC CTA ACC TTA GCT TTG ATT CAC CTG GTC GAA	219
Phe Ala Ala Ser Leu Thr Leu Thr Leu Ala Leu Ile His Leu Val Glu	
15 20 25	
GCA AAC TCC GAA GGA GAT GCT CTC TAC GCT CTT CGC CGG AGT TTG ACA	267
Ala Asn Ser Glu Gly Asp Ala Leu Tyr Ala Leu Arg Arg Ser Leu Thr	
30 35 40	

GAT CCA GAC CAT GTC CTC CAG AGC TGG GAT CCA ACT CTT GTT AAT CCT Asp Pro Asp His Val Leu Gln Ser Trp Asp Pro Thr Leu Val Asn Pro 45 50 55	315
TGT ACC TGG TTC CAT GTC ACC TGT AAC CAA GAC AAC CGC GTC ACT CGT Cys Thr Trp Phe His Val Thr Cys Asn Gln Asp Asn Arg Val Thr Arg 60 65 70	363
GTG GAT TTG GGA AAT TCA AAC CTC TCT GGA CAT CTT GCG CCT GAG CTT Val Asp Leu Gly Asn Ser Asn Leu Ser Gly His Leu Ala Pro Glu Leu 75 80 85 90	411
GGG AAG CTT GAA CAT TTA CAG TAT CTA GAG CTC TAC AAA AAC AAC ATC Gly Lys Leu Glu His Leu Gln Tyr Leu Glu Leu Tyr Lys Asn Asn Ile 95 100 105	459
CAA GGA ACT ATA CCT TCC GAA CTT GGA AAT CTG AAG AAT CTC ATC AGC Gln Gly Thr Ile Pro Ser Glu Leu Gly Asn Leu Lys Asn Leu Ile Ser 110 115 120	507
TTG GAT CTG TAC AAC AAC AAT CTT ACA GGG ATA GTT CCC ACT TTC TTG Leu Asp Leu Tyr Asn Asn Asn Leu Thr Gly Ile Val Pro Thr Phe Leu 125 130 135	555
GGA AAA TTG AAG TCT CTG GTC TTT TTA CGG CTT AAT GAC AAC CGA TTG Gly Lys Leu Lys Ser Leu Val Phe Leu Arg Leu Asn Asp Asn Arg Leu 140 145 150	603
ACC GGT CCA ATC CTA GAG CAC TCA CGG CAA TCC CAA GCC TTT AAA GTT Thr Gly Pro Ile Leu Glu His Ser Arg Gln Ser Gln Ala Phe Lys Val 155 160 165 170	651
GTT GAC GTC TCA AGC AAT GAT TTG TGT GGG ACA ATC CCA ACA AAC GGA Val Asp Val Ser Ser Asn Asp Leu Cys Gly Thr Ile Pro Thr Asn Gly 175 180 185	699
CCC TTT GCT CAC ATT CCT TTA CAG AAC TTT GAG AAC AAC CCG AGA TTG	747

Pro Phe Ala His Ile Pro Leu Gln Asn Phe Glu Asn Asn Pro Arg Leu  
 190 195 200

GAG GGA CCG GAA TTA CTC GGT CTT GCA AGC TAC GAC ACT AAC TGC ACC 795  
 Glu Gly Pro Glu Leu Leu Gly Leu Ala Ser Tyr Asp Thr Asn Cys Thr  
 205 210 215

TGAAACAACCT GGCAAAACCT GAAAATGAAG AATTGGGGGG TGACCTTGTA AGAACACTTC 855

ACCACTTTAT CAAATATCAC ATCTATTATG TAATAAGTAT ATATATGTAG TAAAAACAAA 915

AAAAATGAAG AATOGAATCG GTAATATCAT CTGGTCTCAA TTGAGAACTT CGAGGTCTGT 975

ATGTAAAAAT TCTAAATGCG ATTTTCGCCT ACTGTAATGT TCGGTGTGG GATTCTGAGA 1035

AGTAACATTT GTATTGGTAT GGTATCAAGT TGTCTGCCT TGTCTGCAA AAAAAAAAAA 1095

AAAAAAAAA A 1106

## (2) INFORMATION FOR SEQ ID NO: 23:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

Met Ala Ser Arg Asn Tyr Arg Trp Glu Leu Phe Ala Ala Ser Leu Thr  
 1 5 10 15

Leu Thr Leu Ala Leu Ile His Leu Val Glu Ala Asn Ser Glu Gly Asp  
 20 25 30

Ala Leu Tyr Ala Leu Arg Arg Ser Leu Thr Asp Pro Asp His Val Leu  
 35 40 45

Gln Ser Trp Asp Pro Thr Leu Val Asn Pro Cys Thr Trp Phe His Val  
 50 55 60

Thr Cys Asn Gln Asp Asn Arg Val Thr Arg Val Asp Leu Gly Asn Ser  
 65 70 75 80

Asn Leu Ser Gly His Leu Ala Pro Glu Leu Gly Lys Leu Glu His Leu  
 85 90 95

Gln Tyr Leu Glu Leu Tyr Lys Asn Asn Ile Gln Gly Thr Ile Pro Ser  
 100 105 110

Glu Leu Gly Asn Leu Lys Asn Leu Ile Ser Leu Asp Leu Tyr Asn Asn  
 115 120 125

Asn Leu Thr Gly Ile Val Pro Thr Phe Leu Gly Lys Leu Lys Ser Leu  
 130 135 140

Val Phe Leu Arg Leu Asn Asp Asn Arg Leu Thr Gly Pro Ile Leu Glu  
 145 150 155 160

His Ser Arg Gln Ser Gln Ala Phe Lys Val Val Asp Val Ser Ser Asn  
 165 170 175

Asp Leu Cys Gly Thr Ile Pro Thr Asn Gly Pro Phe Ala His Ile Pro  
 180 185 190

Leu Gln Asn Phe Glu Asn Asn Pro Arg Leu Glu Gly Pro Glu Leu Leu  
 195 200 205

Gly Leu Ala Ser Tyr Asp Thr Asn Cys Thr  
 210 215

(2) INFORMATION FOR SEQ ID NO: 24:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 981 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 104..757

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

```

AGGTGAGTA ATTAGTTTG CTTCCTCTC TTGTTCAGA AAATTTTCCC TTACTCTCA      60
AATTCCTTTT CGATTTCCT CTCTTAAACC TCCGAAAGCT CAC ATG GCG TCT CGA      115
                               Met Ala Ser Arg
                               1
AAC TAT CGG TGG GAG CTC TTC GCA GCT TCG TTA ACC CTA ACC TTA GCT      163
Asn Tyr Arg Trp Glu Leu Phe Ala Ala Ser Leu Thr Leu Thr Leu Ala
  5              10              15              20
TTG ATT CAC CTG GTC GAA GCA AAC TCC GAA GGA GAT GCT CTC TAC GCT      211
Leu Ile His Leu Val Glu Ala Asn Ser Glu Gly Asp Ala Leu Tyr Ala
              25              30              35
CTT CGC CGG AGT TTG ACA GAT CCA GAC CAT GTC CTC CAG AGC TGG GAT      259
Leu Arg Arg Ser Leu Thr Asp Pro Asp His Val Leu Gln Ser Trp Asp
              40              45              50

```

CCA ACT CTT GTT AAT CCT TGT ACC TGG TTC CAT GTC ACC TGT AAC CAA	307
Pro Thr Leu Val Asn Pro Cys Thr Trp Phe His Val Thr Cys Asn Gln	
55 60 65	
GAC AAC CGC GTC ACT CGT GTG GAT TTG GGA AAT TCA AAC CTC TCT GGA	355
Asp Asn Arg Val Thr Arg Val Asp Leu Gly Asn Ser Asn Leu Ser Gly	
70 75 80	
CAT CTT GCG CCT GAG CTT GGG AAG CTT GAA CAT TTA CAG TAT CTA GAG	403
His Leu Ala Pro Glu Leu Gly Lys Leu Glu His Leu Gln Tyr Leu Glu	
85 90 95 100	
CTC TAC AAA AAC AAC ATC CAA GGA ACT ATA CCT TCC GAA CTT GGA AAT	451
Leu Tyr Lys Asn Asn Ile Gln Gly Thr Ile Pro Ser Glu Leu Gly Asn	
105 110 115	
CTG AAG AAT CTC ATC AGC TTG GAT CTG TAC AAC AAC AAT CTT ACA GGG	499
Leu Lys Asn Leu Ile Ser Leu Asp Leu Tyr Asn Asn Asn Leu Thr Gly	
120 125 130	
ATA GTT CCC ACT TCT TTG GGA AAA TTG AAG TCT CTG GTC TTT TTA CGG	547
Ile Val Pro Thr Ser Leu Gly Lys Leu Lys Ser Leu Val Phe Leu Arg	
135 140 145	
CTT AAT GAC AAC CGA TTG ACC GGT CCA ATC CCT AGA GCA CTC ACG GCA	595
Leu Asn Asp Asn Arg Leu Thr Gly Pro Ile Pro Arg Ala Leu Thr Ala	
150 155 160	
ATC CCA AGC CTT AAA GTT GTT GAC GTC TCA AGC AAT GAT TTG TGT GGA	643
Ile Pro Ser Leu Lys Val Val Asp Val Ser Ser Asn Asp Leu Cys Gly	
165 170 175 180	
ACA ATC CCA ACA AAC GGA CCC TTT GCT CAC ATT CCT TTA CAG AAC TTT	691
Thr Ile Pro Thr Asn Gly Pro Phe Ala His Ile Pro Leu Gln Asn Phe	
185 190 195	
GAG AAC AAC CCG AGA TTG GAG GGA CCG GAA TTA CTC GGT CTT GCA AGC	739

Glu Asn Asn Pro Arg Leu Glu Gly Pro Glu Leu Leu Gly Leu Ala Ser  
 200 205 210

TAC GAC ACT AAC TGC ACC TGAAACAACT GGCAAAACCT GAAAATGAAG 787  
 Tyr Asp Thr Asn Cys Thr  
 215

AATTGGGGGG TGACCTTGTA AGAACACTTC ACCACTTTAT CAAATATCAC ATCTATTATG 847

TAATAAGTAT ATATATGTAG TAAAAACAAA AAAAATGAAG AATCGAATCG GTAATATCAT 907

CIGGTCTCAA TTGAGAACTT CGAGGTCTGT ATGTAAAATT TCTAAATGCG ATTTTCGGCT 967

AAATTACTCA CACT 981

## (2) INFORMATION FOR SEQ ID NO: 25:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

Met Ala Ser Arg Asn Tyr Arg Trp Glu Leu Phe Ala Ala Ser Leu Thr  
 1 5 10 15

Leu Thr Leu Ala Leu Ile His Leu Val Glu Ala Asn Ser Glu Gly Asp  
 20 25 30

Ala Leu Tyr Ala Leu Arg Arg Ser Leu Thr Asp Pro Asp His Val Leu  
 35 40 45

Gln Ser Trp Asp Pro Thr Leu Val Asn Pro Cys Thr Trp Phe His Val

50	55	60
Thr Cys Asn Gln Asp Asn Arg Val Thr Arg Val Asp Leu Gly Asn Ser		
65	70	75 80
Asn Leu Ser Gly His Leu Ala Pro Glu Leu Gly Lys Leu Glu His Leu		
	85	90 95
Gln Tyr Leu Glu Leu Tyr Lys Asn Asn Ile Gln Gly Thr Ile Pro Ser		
100	105	110
Glu Leu Gly Asn Leu Lys Asn Leu Ile Ser Leu Asp Leu Tyr Asn Asn		
115	120	125
Asn Leu Thr Gly Ile Val Pro Thr Ser Leu Gly Lys Leu Lys Ser Leu		
130	135	140
Val Phe Leu Arg Leu Asn Asp Asn Arg Leu Thr Gly Pro Ile Pro Arg		
145	150	155 160
Ala Leu Thr Ala Ile Pro Ser Leu Lys Val Val Asp Val Ser Ser Asn		
165	170	175
Asp Leu Cys Gly Thr Ile Pro Thr Asn Gly Pro Phe Ala His Ile Pro		
180	185	190
Leu Gln Asn Phe Glu Asn Asn Pro Arg Leu Glu Gly Pro Glu Leu Leu		
195	200	205
Gly Leu Ala Ser Tyr Asp Thr Asn Cys Thr		
210	215	

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 789 base pairs

(B) TYPE: nucleic acid



(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 2..661

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

T CGA CCC ACG CGT CCG CGA AAC TAT CCG TGG GAG CTC TTC GCA GCT	46
Arg Pro Thr Arg Pro Arg Asn Tyr Arg Trp Glu Leu Phe Ala Ala	
1 5 10 15	
TCG TTA ATC CTA ACC TTA GCT TTG ATT CAC CTG GTC GAA GCA AAC TCC	94
Ser Leu Ile Leu Thr Leu Ala Leu Ile His Leu Val Glu Ala Asn Ser	
20 25 30	
GAA GGA GAT GCT CTT TAC GCT CTT CGC CGG AGT TTA ACA GAT CCG GAC	142
Glu Gly Asp Ala Leu Tyr Ala Leu Arg Arg Ser Leu Thr Asp Pro Asp	
35 40 45	
CAT GTT CTC CAG AGC TGG GAT CCA ACT CTT GTT AAT CCT TGT ACC TGG	190
His Val Leu Gln Ser Trp Asp Pro Thr Leu Val Asn Pro Cys Thr Trp	
50 55 60	
TTC CAT GTC ACC TGT AAC CAA GAC AAC CGC GTC ACT CGT GTG GAT TTG	238
Phe His Val Thr Cys Asn Gln Asp Asn Arg Val Thr Arg Val Asp Leu	
65 70 75	
GGG AAT TCA AAC CTC TCT GGA CAT CTT GCG CCT GAG CTT GGG AAG CTT	286
Gly Asn Ser Asn Leu Ser Gly His Leu Ala Pro Glu Leu Gly Lys Leu	

80	85	90	95	
GAA CAT TTA CAG TAT CTA GAG CTC TAC AAA AAC AAC ATC CAA GGA ACT				334
Glu His Leu Gln Tyr Leu Glu Leu Tyr Lys Asn Asn Ile Gln Gly Thr				
100	105	110		
ATA CCT TCC GAA CTT GGA AAT CTG AAG AAT CTC ATC AGC TTG GAT CTG				382
Ile Pro Ser Glu Leu Gly Asn Leu Lys Asn Leu Ile Ser Leu Asp Leu				
115	120	125		
TAC AAC AAC AAT CTT ACA GGG ATA GTT CCC ACT TCT TTG GGA AAA TTG				430
Tyr Asn Asn Asn Leu Thr Gly Ile Val Pro Thr Ser Leu Gly Lys Leu				
130	135	140		
AAG TCT CTG GTC TTT TTA CGG CTT AAT GAC AAC CGA TTG ACG GGG CCA				478
Lys Ser Leu Val Phe Leu Arg Leu Asn Asp Asn Arg Leu Thr Gly Pro				
145	150	155		
ATC CCT AGA GCA CTC ACT GCA ATC CCA AGC CTT AAA GTT GTT GAT GTC				526
Ile Pro Arg Ala Leu Thr Ala Ile Pro Ser Leu Lys Val Val Asp Val				
160	165	170	175	
TCA AGC AAT GAT TTG TGT GGA ACA ATC CCA ACA AAC GGA CCT TTT GCT				574
Ser Ser Asn Asp Leu Cys Gly Thr Ile Pro Thr Asn Gly Pro Phe Ala				
180	185	190		
CAC ATT CCT TTA CAG AAC TTT GAG AAC AAC CCG AGG TTG GAG GGA CCG				622
His Ile Pro Leu Gln Asn Phe Glu Asn Asn Pro Arg Leu Glu Gly Pro				
195	200	205		
GAA TTA CTC GGT CTT GCA AGC TAC GAC ACT AAC TGC ACC TGAAAAAATT				671
Glu Leu Leu Gly Leu Ala Ser Tyr Asp Thr Asn Cys Thr				
210	215	220		
GGCAAAACCT GAAAATGAAG AATTGGGGGG TGACCTTGTA AGAACACTTC ACCACTTTAT				731
CAATATCAC ATCTACTATG TAATAAGTAT ATATATGTAG TCCAAAAAAA AAAAAAAA				789

## (2) INFORMATION FOR SEQ ID NO: 27:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 220 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

Arg	Pro	Thr	Arg	Pro	Arg	Asn	Tyr	Arg	Trp	Glu	Leu	Phe	Ala	Ala	Ser	1	5	10	15
Leu	Ile	Leu	Thr	Leu	Ala	Leu	Ile	His	Leu	Val	Glu	Ala	Asn	Ser	Glu	20	25	30	
Gly	Asp	Ala	Leu	Tyr	Ala	Leu	Arg	Arg	Ser	Leu	Thr	Asp	Pro	Asp	His	35	40	45	
Val	Leu	Gln	Ser	Trp	Asp	Pro	Thr	Leu	Val	Asn	Pro	Cys	Thr	Trp	Phe	50	55	60	
His	Val	Thr	Cys	Asn	Gln	Asp	Asn	Arg	Val	Thr	Arg	Val	Asp	Leu	Gly	65	70	75	80
Asn	Ser	Asn	Leu	Ser	Gly	His	Leu	Ala	Pro	Glu	Leu	Gly	Lys	Leu	Glu	85	90	95	
His	Leu	Gln	Tyr	Leu	Glu	Leu	Tyr	Lys	Asn	Asn	Ile	Gln	Gly	Thr	Ile	100	105	110	
Pro	Ser	Glu	Leu	Gly	Asn	Leu	Lys	Asn	Leu	Ile	Ser	Leu	Asp	Leu	Tyr	115	120	125	

Asn Asn Asn Leu Thr Gly Ile Val Pro Thr Ser Leu Gly Lys Leu Lys  
130 135 140

Ser Leu Val Phe Leu Arg Leu Asn Asp Asn Arg Leu Thr Gly Pro Ile  
145 150 155 160

Pro Arg Ala Leu Thr Ala Ile Pro Ser Leu Lys Val Val Asp Val Ser  
165 170 175

Ser Asn Asp Leu Cys Gly Thr Ile Pro Thr Asn Gly Pro Phe Ala His  
180 185 190

Ile Pro Leu Gln Asn Phe Glu Asn Asn Pro Arg Leu Glu Gly Pro Glu  
195 200 205

Leu Leu Gly Leu Ala Ser Tyr Asp Thr Asn Cys Thr  
210 215 220

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 894 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..675

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

GGA CCG ATT CAA GCC TCC GAA GGG GAC GCT CTT CAC GCG CTT CGC CGG	48
Gly Pro Ile Gln Ala Ser Glu Gly Asp Ala Leu His Ala Leu Arg Arg	
1 5 10 15	
AGC TTA TCA GAT CCA GAC AAT GTT GTT CAG AGT TGG GAT CCA ACT CTT	96
Ser Leu Ser Asp Pro Asp Asn Val Val Gln Ser Trp Asp Pro Thr Leu	
20 25 30	
GTT AAT CCT TGT ACT TGG TTT CAT GTC ACT TGT AAT CAA CAC CAT CAA	144
Val Asn Pro Cys Thr Trp Phe His Val Thr Cys Asn Gln His His Gln	
35 40 45	
GTC ACT CGT CTG GAT TTG GGG AAT TCA AAC TTA TCT GGA CAT CTA GTA	192
Val Thr Arg Leu Asp Leu Gly Asn Ser Asn Leu Ser Gly His Leu Val	
50 55 60	
CCT GAA CTT GGG AAG CTT GAA CAT TTA CAA TAT CTG TAT GGA ATC ATC	240
Pro Glu Leu Gly Lys Leu Glu His Leu Gln Tyr Leu Tyr Gly Ile Ile	
65 70 75 80	
ACT CTT TTG CCT TTT GAT TAT CTG AAA ACA TTT ACA TTA TCA GTC ACA	288
Thr Leu Leu Pro Phe Asp Tyr Leu Lys Thr Phe Thr Leu Ser Val Thr	
85 90 95	
CAT ATA ACA TTT TGC TTT GAG TCA TAT AGT GAA CTC TAC AAA AAC GAG	336
His Ile Thr Phe Cys Phe Glu Ser Tyr Ser Glu Leu Tyr Lys Asn Glu	
100 105 110	
ATT CAA GGA ACT ATA CCT TCT GAG CTT GGA AAT CTG AAG AGT CTA ATC	384
Ile Gln Gly Thr Ile Pro Ser Glu Leu Gly Asn Leu Lys Ser Leu Ile	
115 120 125	
AGT TTG GAT CTG TAC AAC AAC AAT CTC ACC GGG AAA ATC CCA TCT TCT	432
Ser Leu Asp Leu Tyr Asn Asn Asn Leu Thr Gly Lys Ile Pro Ser Ser	
130 135 140	

TTG GGA AAA TTG AAG TCA CTT GTT TTT TTG CGG CTT AAC GAA AAC CGA	480
Leu Gly Lys Leu Lys Ser Leu Val Phe Leu Arg Leu Asn Glu Asn Arg	
145                                      150                                      155                                      160	
TTG ACC GGT CCT ATT CCT AGA GAA CTC ACA GTT ATT TCA AGC CTT AAA	528
Leu Thr Gly Pro Ile Pro Arg Glu Leu Thr Val Ile Ser Ser Leu Lys	
165                                      170                                      175	
GTT GTT GAT GTC TCA GGG AAT GAT TTG TGT GGA ACA ATT CCA GTA GAA	576
Val Val Asp Val Ser Gly Asn Asp Leu Cys Gly Thr Ile Pro Val Glu	
180                                      185                                      190	
GGA CCT TTT GAA CAC ATT CCT ATG CAA AAC TTT GAG AAC AAC CTG AGA	624
Gly Pro Phe Glu His Ile Pro Met Gln Asn Phe Glu Asn Asn Leu Arg	
195                                      200                                      205	
TTG GAG GGA CCA GAA CTA CTA GGT CTT GCG AGC TAT GAC ACC AAT TGC	672
Leu Glu Gly Pro Glu Leu Leu Gly Leu Ala Ser Tyr Asp Thr Asn Cys	
210                                      215                                      220	
ACT TAAAAGAAG TTGAAGAACC TATAAGAAG AATGTTAGGT GACCTTGTA	725
Thr	
225	
GAAGTCTGTA CCAAGTGTTT GTAAATCTAT ATAGAGCCTT GTTCATGTT ATATATGAAA	785
GCCTTGAGAG ACAGTAACCT GCAATGTATT GGTATTGGTA GAAAAAGTTG AAATGAGAAT	845
TGCTTTGTAA TTGGATTGT GTTCTTATG TAACTTGAAT TTCTTATTA	894

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

Gly Pro Ile Gln Ala Ser Glu Gly Asp Ala Leu His Ala Leu Arg Arg  
 1 5 10 15  
 Ser Leu Ser Asp Pro Asp Asn Val Val Gln Ser Trp Asp Pro Thr Leu  
 20 25 30  
 Val Asn Pro Cys Thr Trp Phe His Val Thr Cys Asn Gln His His Gln  
 35 40 45  
 Val Thr Arg Leu Asp Leu Gly Asn Ser Asn Leu Ser Gly His Leu Val  
 50 55 60  
 Pro Glu Leu Gly Lys Leu Glu His Leu Gln Tyr Leu Tyr Gly Ile Ile  
 65 70 75 80  
 Thr Leu Leu Pro Phe Asp Tyr Leu Lys Thr Phe Thr Leu Ser Val Thr  
 85 90 95  
 His Ile Thr Phe Cys Phe Glu Ser Tyr Ser Glu Leu Tyr Lys Asn Glu  
 100 105 110  
 Ile Gln Gly Thr Ile Pro Ser Glu Leu Gly Asn Leu Lys Ser Leu Ile  
 115 120 125  
 Ser Leu Asp Leu Tyr Asn Asn Asn Leu Thr Gly Lys Ile Pro Ser Ser  
 130 135 140  
 Leu Gly Lys Leu Lys Ser Leu Val Phe Leu Arg Leu Asn Glu Asn Arg  
 145 150 155 160  
 Leu Thr Gly Pro Ile Pro Arg Glu Leu Thr Val Ile Ser Ser Leu Lys  
 165 170 175

Val Val Asp Val Ser Gly Asn Asp Leu Cys Gly Thr Ile Pro Val Glu  
 180 185 190

Gly Pro Phe Glu His Ile Pro Met Gln Asn Phe Glu Asn Asn Leu Arg  
 195 200 205

Leu Glu Gly Pro Glu Leu Leu Gly Leu Ala Ser Tyr Asp Thr Asn Cys  
 210 215 220

Thr  
 225

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1063 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 106..759

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

TOGACCCACG CGTCGACGA AACCCCTAATT TTGCTTCCTC ATCTTGTTCA GAAAATTACT 60  
 CAAATTCCTA TTAGATTACT CTCTCTTGA CCTCCGATAG CTCAC ATG GCG TCT 114  
 Met Ala Ser



1

CGA AAC TAT OGG TGG GAG CTC TTC GCA GCT TCG TTA ATC CTA ACC TTA	162
Arg Asn Tyr Arg Trp Glu Leu Phe Ala Ala Ser Leu Ile Leu Thr Leu	
5 10 15	
GCT TTG ATT CAC CTG GTC GAA GCA AAC TCC GAA GGA GAT GCT CTT TAC	210
Ala Leu Ile His Leu Val Glu Ala Asn Ser Glu Gly Asp Ala Leu Tyr	
20 25 30 35	
GCT CTT CGC OGG AGT TTA ACA GAT CCG GAC CAT GTT CTC CAG AGC TGG	258
Ala Leu Arg Arg Ser Leu Thr Asp Pro Asp His Val Leu Gln Ser Trp	
40 45 50	
GAT CCA ACT CTT GTT AAT CCT TGT ACC TGG TTC CAT GTC ACC TGT AAC	306
Asp Pro Thr Leu Val Asn Pro Cys Thr Trp Phe His Val Thr Cys Asn	
55 60 65	
CAA GAC AAC CGC GTC ACT CGT GTG GAT TTG GGG AAT TCA AAC CTC TCT	354
Gln Asp Asn Arg Val Thr Arg Val Asp Leu Gly Asn Ser Asn Leu Ser	
70 75 80	
GGA CAT CTT GCG CCT GAG CTT GGG AAG CTT GAA CAT TTA CAG TAT CTA	402
Gly His Leu Ala Pro Glu Leu Gly Lys Leu Glu His Leu Gln Tyr Leu	
85 90 95	
GAG CTC TAC AAA AAC AAC ATC CAA GGA ACT ATA CCT TCC GAA CTT GGA	450
Glu Leu Tyr Lys Asn Asn Ile Gln Gly Thr Ile Pro Ser Glu Leu Gly	
100 105 110 115	
AAT CTG AAG AAT CTC ATC AGC TTG GAT CTG TAC AAC AAC AAT CTT ACA	498
Asn Leu Lys Asn Leu Ile Ser Leu Asp Leu Tyr Asn Asn Asn Leu Thr	
120 125 130	
GGG ATA GTT CCC ACT TCT TTG GGA AAA TTG AAG TCT CTG GTC TTT TTA	546
Gly Ile Val Pro Thr Ser Leu Gly Lys Leu Lys Ser Leu Val Phe Leu	
135 140 145	

CGG CTT AAT GAC AAC CGA TTG ACG GGG CCA ATC CCT AGA GCA CTC ACT	594
Arg Leu Asn Asp Asn Arg Leu Thr Gly Pro Ile Pro Arg Ala Leu Thr	
150 155 160	
GCA ATC CCA AGC CTT AAA GTT GTT GAT GTC TCA AGC AAT GAT TTG TGT	642
Ala Ile Pro Ser Leu Lys Val Val Asp Val Ser Ser Asn Asp Leu Cys	
165 170 175	
GGA ACA ATC CCA ACA AAC GGA CCT TTT GCT CAC ATT CCT TTA CAG AAC	690
Gly Thr Ile Pro Thr Asn Gly Pro Phe Ala His Ile Pro Leu Gln Asn	
180 185 190 195	
TTT GAG AAC AAC CCG AGG TTG GAG GGA CCG GAA TTA CTC GGT CTT GCA	738
Phe Glu Asn Asn Pro Arg Leu Glu Gly Pro Glu Leu Leu Gly Leu Ala	
200 205 210	
AGC TAC GAC ACT AAC TGC ACC TGAAAAAATT GGCAAAACCT GAAAATGAAG	789
Ser Tyr Asp Thr Asn Cys Thr	
215	
AATGGGGGGG TGACCTTGTA AGAACACTTC ACCACTTTAT CAAATATCAC ATCTACTATG	849
TAATAAGTAT ATATATGTAG TCCAAAAAAA AAATGAAGAA TCGAATCAGT AATATCATCT	909
GGTCTCAATT GAGAACTTTG AGGTCTGTGT ATGTAAAATT TCTAAATGCG ACTTTGCGGT	969
ACTGTAATGT TCGGTTGTGG GATTCTGAGA AGTAACATTT GTATTGGTAT GGTATCAAGT	1029
TGTTCTGCCT TGCTGCAAA AAAAAAAAAA AAAA	1063

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 218 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

Met Ala Ser Arg Asn Tyr Arg Trp Glu Leu Phe Ala Ala Ser Leu Ile  
1 5 10 15

Leu Thr Leu Ala Leu Ile His Leu Val Glu Ala Asn Ser Glu Gly Asp  
20 25 30

Ala Leu Tyr Ala Leu Arg Arg Ser Leu Thr Asp Pro Asp His Val Leu  
35 40 45

Gln Ser Trp Asp Pro Thr Leu Val Asn Pro Cys Thr Trp Phe His Val  
50 55 60

Thr Cys Asn Gln Asp Asn Arg Val Thr Arg Val Asp Leu Gly Asn Ser  
65 70 75 80

Asn Leu Ser Gly His Leu Ala Pro Glu Leu Gly Lys Leu Glu His Leu  
85 90 95

Gln Tyr Leu Glu Leu Tyr Lys Asn Asn Ile Gln Gly Thr Ile Pro Ser  
100 105 110

Glu Leu Gly Asn Leu Lys Asn Leu Ile Ser Leu Asp Leu Tyr Asn Asn  
115 120 125

Asn Leu Thr Gly Ile Val Pro Thr Ser Leu Gly Lys Leu Lys Ser Leu  
130 135 140

Val Phe Leu Arg Leu Asn Asp Asn Arg Leu Thr Gly Pro Ile Pro Arg  
145 150 155 160

Ala Leu Thr Ala Ile Pro Ser Leu Lys Val Val Asp Val Ser Ser Asn

165 170 175  
Asp Leu Cys Gly Thr Ile Pro Thr Asn Gly Pro Phe Ala His Ile Pro  
180 185 190  
Leu Gln Asn Phe Glu Asn Asn Pro Arg Leu Glu Gly Pro Glu Leu Leu  
195 200 205  
Gly Leu Ala Ser Tyr Asp Thr Asn Cys Thr  
210 215

## (2) INFORMATION FOR SEQ ID NO: 32:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2089 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA to mRNA

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Arabidopsis thaliana

## (vii) IMMEDIATE SOURCE:

- (B) CLONE: SERK gene cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 195..2069

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

GGATTTTAT TTTATTTTTT ACTCTTTGTT TGTTTTAATG CTAATGGGT TTTAAAAGG	60
TTATCGAAAA AATGAGTGAG TTGTGTGTA GGTGTCTCT GTAAAGTGT AATGGTGGTG	120
ATTTTCGGAA GTTAGGGTT TCTCGGATCT GAAGAGATCA AATCAAGATT CGAAATTTAC	180
CATTGTGTT TGAA ATG GAG TCG AGT TAT GTG GTG TTT ATC TTA CTT TCA	230
Met Glu Ser Ser Tyr Val Val Phe Ile Leu Leu Ser	
1 5 10	
CTG ATC TTA CTT CCG AAT CAT TCA CTG TGG CTT GCT TCT GCT AAT TTG	278
Leu Ile Leu Leu Pro Asn His Ser Leu Trp Leu Ala Ser Ala Asn Leu	
15 20 25	
GAA GGT GAT GCT TTG CAT ACT TTG AGG GTT ACT CTA GTT GAT CCA AAC	326
Glu Gly Asp Ala Leu His Thr Leu Arg Val Thr Leu Val Asp Pro Asn	
30 35 40	
AAT GTC TTG CAG AGC TGG GAT OCT ACG CTA GTG AAT OCT TGC ACA TGG	374
Asn Val Leu Gln Ser Trp Asp Pro Thr Leu Val Asn Pro Cys Thr Trp	
45 50 55 60	
TTC CAT GTC ACT TGC AAC AAC GAG AAC AGT GTC ATA AGA GTT GAT TTG	422
Phe His Val Thr Cys Asn Asn Glu Asn Ser Val Ile Arg Val Asp Leu	
65 70 75	
GGG AAT GCA GAG TTA TCT GGC CAT TTA GTT CCA GAG CTT GGT GTG CTC	470
Gly Asn Ala Glu Leu Ser Gly His Leu Val Pro Glu Leu Gly Val Leu	
80 85 90	
AAG AAT TTG CAG TAT TTG GAG CTT TAC AGT AAC AAC ATA ACT GGC CCG	518
Lys Asn Leu Gln Tyr Leu Glu Leu Tyr Ser Asn Asn Ile Thr Gly Pro	
95 100 105	
ATT OCT AGT AAT CTT GGA AAT CTG ACA AAC TTA GTG AGT TTG GAT CTT	566

Ile Pro Ser Asn Leu Gly Asn Leu Thr Asn Leu Val Ser Leu Asp Leu	
110                                      115                                      120	
TAC TTA AAC AGC TTC TCC GGT CCT ATT CCG GAA TCA TTG GGA AAG CTT	614
Tyr Leu Asn Ser Phe Ser Gly Pro Ile Pro Glu Ser Leu Gly Lys Leu	
125                                      130                                      135                                      140	
TCA AAG CTG AGA TTT CTC CGG CTT AAC AAC AAC AGT CTC ACT GGG TCA	662
Ser Lys Leu Arg Phe Leu Arg Leu Asn Asn Asn Ser Leu Thr Gly Ser	
145                                      150                                      155	
ATT CCT ATG TCA CTG ACC AAT ATT ACT ACC CTT CAA GTG TTA GAT CTA	710
Ile Pro Met Ser Leu Thr Asn Ile Thr Thr Leu Gln Val Leu Asp Leu	
160                                      165                                      170	
TCA AAT AAC AGA CTC TCT GGT TCA GTT CCT GAC AAT GGC TCC TTC TCA	758
Ser Asn Asn Arg Leu Ser Gly Ser Val Pro Asp Asn Gly Ser Phe Ser	
175                                      180                                      185	
CTC TTC ACA CCC ATC AGT TTT GCT AAT AAC TTA GAC CTA TGT GGA CCT	806
Leu Phe Thr Pro Ile Ser Phe Ala Asn Asn Leu Asp Leu Cys Gly Pro	
190                                      195                                      200	
GTT ACA AGT CAC CCA TGT CCT GGA TCT CCC CCG TTT TCT CCT CCA CCA	854
Val Thr Ser His Pro Cys Pro Gly Ser Pro Pro Phe Ser Pro Pro Pro	
205                                      210                                      215                                      220	
CCT TTT ATT CAA CCT CCC CCA GTT TCC ACC CCG AGT GGG TAT GGT ATA	902
Pro Phe Ile Gln Pro Pro Pro Val Ser Thr Pro Ser Gly Tyr Gly Ile	
225                                      230                                      235	
ACT GGA GCA ATA GCT GGT GGA GTT GCT GCA GGT GCT GCT TTG CCC TTT	950
Thr Gly Ala Ile Ala Gly Gly Val Ala Ala Gly Ala Ala Leu Pro Phe	
240                                      245                                      250	
GCT GCT CCT GCA ATA GCC TTT GCT TGG TGG CGA CGA AGA AGC CCA CTA	998
Ala Ala Pro Ala Ile Ala Phe Ala Trp Trp Arg Arg Arg Ser Pro Leu	

255	260	265	
GAT ATT TTC TTC GAT GTC OCT GCC GAA GAA GAT CCA GAA GTT CAT CTG			1046
Asp Ile Phe Phe Asp Val Pro Ala Glu Glu Asp Pro Glu Val His Leu			
270	275	280	
GGA CAG CTC AAG AGG TTT TCT TTG CGG GAG CTA CAA GTG GCG AGT GAT			1094
Gly Gln Leu Lys Arg Phe Ser Leu Arg Glu Leu Gln Val Ala Ser Asp			
285	290	295	300
GGG TTT AGT AAC AAG AAC ATT TTG GGC AGA GGT GGG TTT GGG AAA GTC			1142
Gly Phe Ser Asn Lys Asn Ile Leu Gly Arg Gly Gly Phe Gly Lys Val			
305	310	315	
TAC AAG GGA CGC TTG GCA GAC GGA ACT CTT GTT GCT GTC AAG AGA CTG			1190
Tyr Lys Gly Arg Leu Ala Asp Gly Thr Leu Val Ala Val Lys Arg Leu			
320	325	330	
AAG GAA GAG CGA ACT CCA GGT GGA GAG CTC CAG TTT CAA ACA GAA GTA			1238
Lys Glu Glu Arg Thr Pro Gly Gly Glu Leu Gln Phe Gln Thr Glu Val			
335	340	345	
GAG ATG ATA AGT ATG GCA GTT CAT CGA AAC CTG TTG AGA TTA CGA GGT			1286
Glu Met Ile Ser Met Ala Val His Arg Asn Leu Leu Arg Leu Arg Gly			
350	355	360	
TTC TGT ATG ACA CCG ACC GAG AGA TTG CTT GTG TAT CCT TAC ATG GCC			1334
Phe Cys Met Thr Pro Thr Glu Arg Leu Leu Val Tyr Pro Tyr Met Ala			
365	370	375	380
AAT GGA AGT GTT GCT TCG TGT CTC AGA GAG AGG CCA CCG TCA CAA CCT			1382
Asn Gly Ser Val Ala Ser Cys Leu Arg Glu Arg Pro Pro Ser Gln Pro			
385	390	395	
CCG CTT GAT TGG CCA ACG CGG AAG AGA ATC GCG CTA GGC TCA GCT CGA			1430
Pro Leu Asp Trp Pro Thr Arg Lys Arg Ile Ala Leu Gly Ser Ala Arg			
400	405	410	

GGT TTG TCT TAC CTA CAT GAT CAC TGC GAT CCG AAG ATC ATT CAC CGT Gly Leu Ser Tyr Leu His Asp His Cys Asp Pro Lys Ile Ile His Arg 415 420 425	1478
GAC GTA AAA GCA GCA AAC ATC CTC TTA GAC GAA GAA TTC GAA GCG GTT Asp Val Lys Ala Ala Asn Ile Leu Leu Asp Glu Glu Phe Glu Ala Val 430 435 440	1526
GTT GGA GAT TTC GGG TTG GCA AAG CTT ATG GAC TAT AAA GAC ACT CAC Val Gly Asp Phe Gly Leu Ala Lys Leu Met Asp Tyr Lys Asp Thr His 445 450 455 460	1574
GTG ACA ACA GCA GTC CGT GGC ACC ATC GGT CAC ATC GCT CCA GAA TAT Val Thr Thr Ala Val Arg Gly Thr Ile Gly His Ile Ala Pro Glu Tyr 465 470 475	1622
CTC TCA ACC GGA AAA TCT TCA GAG AAA ACC GAC GTT TTC GGA TAC GGA Leu Ser Thr Gly Lys Ser Ser Glu Lys Thr Asp Val Phe Gly Tyr Gly 480 485 490	1670
ATC ATG CTT CTA GAA CTA ATC ACA GGA CAA AGA GCT TTC GAT CTC GCT Ile Met Leu Leu Glu Leu Ile Thr Gly Gln Arg Ala Phe Asp Leu Ala 495 500 505	1718
CGG CTA GCT AAC GAC GAC GAC GTC ATG TTA CTT GAC TGG GTG AAA GGA Arg Leu Ala Asn Asp Asp Asp Val Met Leu Leu Asp Trp Val Lys Gly 510 515 520	1766
TTG TTG AAG GAG AAG AAG CTA GAG ATG TTA GTG GAT CCA GAT CTT CAA Leu Leu Lys Glu Lys Lys Leu Glu Met Leu Val Asp Pro Asp Leu Gln 525 530 535 540	1814
ACA AAC TAC GAG GAG AGA GAA CTG GAA CAA GTG ATA CAA GTG GCG TTG Thr Asn Tyr Glu Glu Arg Glu Leu Glu Gln Val Ile Gln Val Ala Leu 545 550 555	1862



CTA TGC ACG CAA GGA TCA CCA ATG GAA AGA CCA AAG ATG TCT GAA GTT 1910  
 Leu Cys Thr Gln Gly Ser Pro Met Glu Arg Pro Lys Met Ser Glu Val  
 560 565 570

GTA AGG ATG CTG GAA GGA GAT GGG CTT GCG GAG AAA TGG GAC GAA TGG 1958  
 Val Arg Met Leu Glu Gly Asp Gly Leu Ala Glu Lys Trp Asp Glu Trp  
 575 580 585

CAA AAA GTT GAG ATT TTG AGG GAA GAG ATT GAT TTG AGT CCT AAT CCT 2006  
 Gln Lys Val Glu Ile Leu Arg Glu Glu Ile Asp Leu Ser Pro Asn Pro  
 590 595 600

AAC TCT GAT TGG ATT CTT GAT TCT ACT TAC AAT TTG CAC GCC GTT GAG 2054  
 Asn Ser Asp Trp Ile Leu Asp Ser Thr Tyr Asn Leu His Ala Val Glu  
 605 610 615 620

TTA TCT GGT CCA AGG TAAAAAAAA AAAAAAAAAA 2089  
 Leu Ser Gly Pro Arg  
 625

## (2) INFORMATION FOR SEQ ID NO: 33:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 625 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

Met Glu Ser Ser Tyr Val Val Phe Ile Leu Leu Ser Leu Ile Leu Leu  
 1 5 10 15

Pro Asn His Ser Leu Trp Leu Ala Ser Ala Asn Leu Glu Gly Asp Ala  
 20 25 30

Leu His Thr Leu Arg Val Thr Leu Val Asp Pro Asn Asn Val Leu Gln  
 35 40 45

Ser Trp Asp Pro Thr Leu Val Asn Pro Cys Thr Trp Phe His Val Thr  
 50 55 60

Cys Asn Asn Glu Asn Ser Val Ile Arg Val Asp Leu Gly Asn Ala Glu  
 65 70 75 80

Leu Ser Gly His Leu Val Pro Glu Leu Gly Val Leu Lys Asn Leu Gln  
 85 90 95

Tyr Leu Glu Leu Tyr Ser Asn Asn Ile Thr Gly Pro Ile Pro Ser Asn  
 100 105 110

Leu Gly Asn Leu Thr Asn Leu Val Ser Leu Asp Leu Tyr Leu Asn Ser  
 115 120 125

Phe Ser Gly Pro Ile Pro Glu Ser Leu Gly Lys Leu Ser Lys Leu Arg  
 130 135 140

Phe Leu Arg Leu Asn Asn Asn Ser Leu Thr Gly Ser Ile Pro Met Ser  
 145 150 155 160

Leu Thr Asn Ile Thr Thr Leu Gln Val Leu Asp Leu Ser Asn Asn Arg  
 165 170 175

Leu Ser Gly Ser Val Pro Asp Asn Gly Ser Phe Ser Leu Phe Thr Pro  
 180 185 190

Ile Ser Phe Ala Asn Asn Leu Asp Leu Cys Gly Pro Val Thr Ser His  
 195 200 205

Pro Cys Pro Gly Ser Pro Pro Phe Ser Pro Pro Pro Phe Ile Gln  
 210 215 220

Pro Pro Pro Val Ser Thr Pro Ser Gly Tyr Gly Ile Thr Gly Ala Ile  
 225                      230                      235                      240

Ala Gly Gly Val Ala Ala Gly Ala Ala Leu Pro Phe Ala Ala Pro Ala  
                     245                      250                      255

Ile Ala Phe Ala Trp Trp Arg Arg Arg Ser Pro Leu Asp Ile Phe Phe  
                     260                      265                      270

Asp Val Pro Ala Glu Glu Asp Pro Glu Val His Leu Gly Gln Leu Lys  
                     275                      280                      285

Arg Phe Ser Leu Arg Glu Leu Gln Val Ala Ser Asp Gly Phe Ser Asn  
                     290                      295                      300

Lys Asn Ile Leu Gly Arg Gly Gly Phe Gly Lys Val Tyr Lys Gly Arg  
 305                      310                      315                      320

Leu Ala Asp Gly Thr Leu Val Ala Val Lys Arg Leu Lys Glu Glu Arg  
                     325                      330                      335

Thr Pro Gly Gly Glu Leu Gln Phe Gln Thr Glu Val Glu Met Ile Ser  
                     340                      345                      350

Met Ala Val His Arg Asn Leu Leu Arg Leu Arg Gly Phe Cys Met Thr  
                     355                      360                      365

Pro Thr Glu Arg Leu Leu Val Tyr Pro Tyr Met Ala Asn Gly Ser Val  
                     370                      375                      380

Ala Ser Cys Leu Arg Glu Arg Pro Pro Ser Gln Pro Pro Leu Asp Trp  
 385                      390                      395                      400

Pro Thr Arg Lys Arg Ile Ala Leu Gly Ser Ala Arg Gly Leu Ser Tyr  
                     405                      410                      415

Leu His Asp His Cys Asp Pro Lys Ile Ile His Arg Asp Val Lys Ala

420	425	430
Ala Asn Ile Leu Leu Asp Glu Glu Phe Glu Ala Val Val Gly Asp Phe		
435	440	445
Gly Leu Ala Lys Leu Met Asp Tyr Lys Asp Thr His Val Thr Thr Ala		
450	455	460
Val Arg Gly Thr Ile Gly His Ile Ala Pro Glu Tyr Leu Ser Thr Gly		
465	470	475
		480
Lys Ser Ser Glu Lys Thr Asp Val Phe Gly Tyr Gly Ile Met Leu Leu		
485	490	495
Glu Leu Ile Thr Gly Gln Arg Ala Phe Asp Leu Ala Arg Leu Ala Asn		
500	505	510
Asp Asp Asp Val Met Leu Leu Asp Trp Val Lys Gly Leu Leu Lys Glu		
515	520	525
Lys Lys Leu Glu Met Leu Val Asp Pro Asp Leu Gln Thr Asn Tyr Glu		
530	535	540
Glu Arg Glu Leu Glu Gln Val Ile Gln Val Ala Leu Leu Cys Thr Gln		
545	550	555
		560
Gly Ser Pro Met Glu Arg Pro Lys Met Ser Glu Val Val Arg Met Leu		
565	570	575
Glu Gly Asp Gly Leu Ala Glu Lys Trp Asp Glu Trp Gln Lys Val Glu		
580	585	590
Ile Leu Arg Glu Glu Ile Asp Leu Ser Pro Asn Pro Asn Ser Asp Trp		
595	600	605
Ile Leu Asp Ser Thr Tyr Asn Leu His Ala Val Glu Leu Ser Gly Pro		
610	615	620

Arg

625

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**What is Claimed is:**

1. A method of producing apomictic seeds comprising the steps of:
  - (i) transforming plant material with a nucleotide sequence encoding a protein the presence of which in an active form in a cell, or membrane thereof, renders said cell embryogenic,
  - (ii) regenerating the thus transformed material into plants, or carpel-containing parts thereof, and
  - (iii) expressing the sequence in the vicinity of the embryo sac.
2. A method according to the preceding claim, wherein the apomictic seeds are of the adventitious embryony type.
3. A method according to either of the preceding claims, wherein expression of the sequence yields a protein kinase capable of spanning a plant cell membrane.
4. A method according to the preceding claim wherein the kinase is capable of autophosphorylation.
5. A method according to any of the preceding claims, wherein the protein is a leucine rich repeat receptor like kinase and comprises a ligand binding domain, a proline box, a transmembrane domain, a kinase domain and a protein binding domain.
6. A method according to the preceding claim, wherein the protein lacks a functional ligand binding domain but comprises a proline box, a transmembrane domain, a kinase domain and a protein binding domain.
7. A method according to any preceding claim, wherein once incorporated into the cell membrane, the protein binding domain is located intra-cellularly.
8. A method according to any preceding claim, wherein the sequence further encodes a cell membrane targeting sequence.

9. A method according to any preceding claim, wherein the sequence is that depicted in SEQ ID Nos. 1 or 2 or is complementary to one which hybridizes under stringent conditions with the said sequences and which encodes a membrane bound protein having kinase activity.
10. A method according to any preceding claim, wherein the sequence is modified in that known mRNA instability motifs or polyadenylation signals are removed and/or codons which are preferred by the plant into which the sequence is to be inserted are used so that expression of the thus modified sequence in the said plant yields substantially similar protein to that obtained by expression of the unmodified sequence in the organism in which the protein is endogenous.
11. A method according to any preceding claim, wherein expression of the sequence is under control of an inducible or developmentally regulated promoter.
12. A method according to the preceding claim, wherein expression of the sequence is under control of one of the following: a promoter which regulates expression of SERK genes *in planta*, the carrot chitinase DcEP3-1 gene promoter, the *Arabidopsis* AtChitIV gene promoter, the *Arabidopsis* LTP-1 gene promoter, the *Arabidopsis* bel-1 gene promoter, the petunia fbp-7 gene promoter, the *Arabidopsis* ANT gene promoter, the promoter of the O126 gene from *Phalaenopsis*.
13. A method according to any of the preceding claims, wherein the sequence is expressed in the somatic cells of the embryo sac, ovary wall, nucellus, or integuments.
14. A method according to any of the preceding claims, wherein the endosperm within the apomictic seed results from fusion of polar nuclei within the embryo sac with a pollen-derived male gamete nucleus.
15. A method according to the preceding claim, wherein the sequence encoding the protein is expressed prior to fusion of the polar nuclei with the male gamete nucleus.

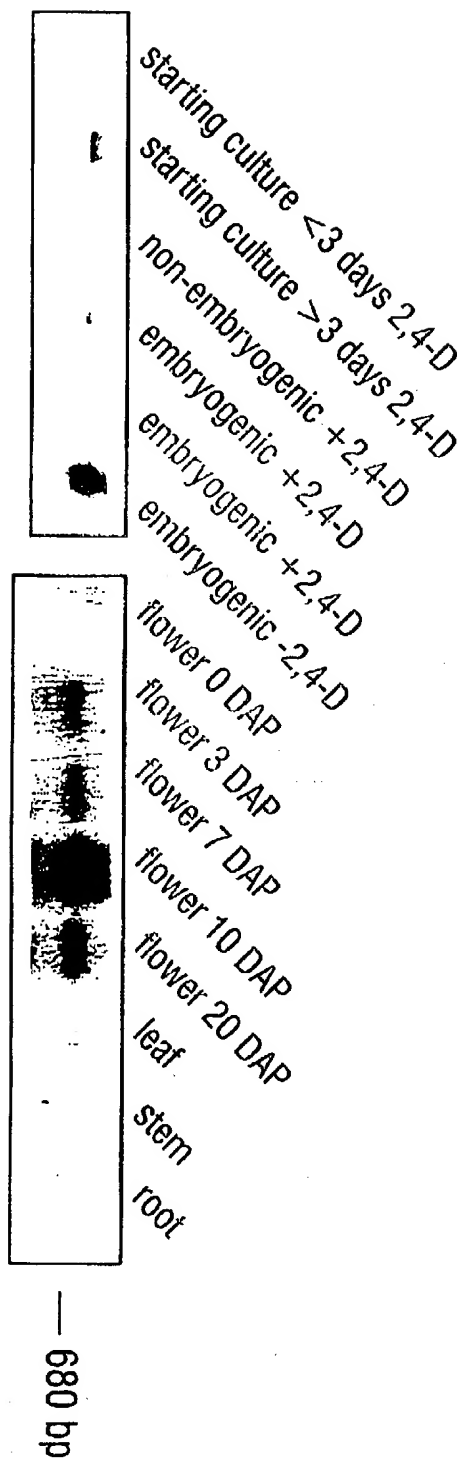
16. DNA comprising a sequence encoding a protein the presence of which in an active form in a cell, or membrane thereof, renders said cell embryogenic.
17. DNA according to claim 16, wherein the protein is a leucine rich repeat receptor like kinase and comprises a ligand binding domain, a proline box, a transmembrane domain, a kinase domain and a protein binding domain, the ligand binding domain optionally being absent or functionally inactive.
18. DNA according to either of claims 16 or 17 comprising a DNA sequence encoding a N-terminal protein fragment having the following amino acid sequence: Gln Ser Trp Asp Pro Thr Leu Val Asn Pro Cys Thr Trp Phe His Val Thr Cys Asn.
19. DNA according to claim 18 comprising a DNA sequence encoding a N-terminal protein fragment having the following amino acid sequence: Val Xaa Gln Ser Trp Asp Pro Thr Leu Val Asn Pro Cys Thr Trp Phe His Val Thr Cys Asn  
with Xaa being a variable amino acid, but preferably Leu or Val
20. DNA according to claim 19 comprising a DNA sequence encoding a N-terminal protein fragment having the following amino acid sequence: Val Xaa Gln Ser Trp Asp Pro Thr Leu Val Asn Pro Cys Thr Trp Phe His Val Thr Cys Asn Xab Xac Xad Xae Val Xaf Arg Val Asp Leu Gly Asn Xag Xah Leu Ser Gly His Leu Xai Pro Glu Leu Gly Xaj Leu Xak Xal Leu Gln  
with Xaa to Xak being a variable amino acid, but preferably  
 Xaa = Leu or Val  
 Xab = Asn or Gln  
 Xac = Glu or Asp or His  
 Xad = Asn or His  
 Xae = Ser or Arg or Gln  
 Xaf = Ile or Thr  
 Xag = Ala or Ser  
 Xah = Glu or Asn  
 Xai = Val or Ala  
 Xaj = Val or Lys  
 Xak = Lys or Glu

Xal = Asn or His

21. DNA comprising a sequence encoding a protein having the sequence depicted in SEQ ID No. 3, or a protein substantially similar thereto which is capable of being membrane bound and which has kinase activity.
22. DNA comprising a sequence encoding a protein having the sequence depicted in SEQ ID No. 21, or a protein substantially similar thereto which is capable of being membrane bound and which has kinase activity.
23. DNA comprising a sequence encoding a protein having the sequence depicted in SEQ ID No. 33, or a protein substantially similar thereto which is capable of being membrane bound and which has kinase activity.
24. DNA comprising a sequence encoding a protein having the sequence depicted in SEQ ID Nos. 23, 25, 27, 29 and 31, or a protein substantially similar thereto which is capable of being membrane bound and which has kinase activity.
25. DNA according to any preceding claim, comprising a DNA having the sequence depicted in SEQ ID Nos. 1 or 2 or a sequence which is complementary to one which hybridizes under stringent conditions with the said sequences and which encodes a membrane bound protein having kinase activity.
26. DNA according to any preceding claim, comprising a DNA having the sequence depicted in SEQ ID No: 20 or a sequence which is complementary to one which hybridizes under stringent conditions with the said sequences and which encodes a membrane bound protein having kinase activity.
27. DNA according to any preceding claim, comprising a DNA having the sequence depicted in SEQ ID No: 32 or a sequence which is complementary to one which hybridizes under stringent conditions with the said sequences and which encodes a membrane bound protein having kinase activity.

28. DNA according to any preceding claim, comprising a DNA having the sequence depicted in SEQ ID Nos: 22, 24, 26, 28 and 30 or a sequence which is complementary to one which hybridizes under stringent conditions with the said sequences and which encodes a membrane bound protein having kinase activity.
29. DNA according to any of the preceding claims, which further encodes a cell membrane targeting sequence.
30. DNA according to any one of the preceding claims, in which the protein encoding region is under expression control of a developmentally regulated or inducible promoter.
31. DNA according to claim 30, wherein the promoter is one of the following: a promoter which regulates expression of SERK genes *in planta*, the carrot chitinase DcEP3-1 gene promoter, the *Arabidopsis* AtChitIV gene promoter, the *Arabidopsis* LTP-1 gene promoter, the *Arabidopsis* bel-1 gene promoter, the petunia fbp-7 gene promoter, the *Arabidopsis* ANT gene promoter, the promoter of the O126 gene from *Phalaenopsis*; the *Arabidopsis* DMC1 promoter, the pTA7001 inducible promoter.
32. DNA according to any preceding claim, wherein said DNA is a recombinant DNA.
33. DNA according to any preceding claim, wherein the sequence is modified in that known mRNA instability motifs or polyadenylation signals are removed and/or codons which are preferred by the plant into which the DNA is to be inserted are used so that expression of the thus modified DNA in the said plant yields substantially similar protein to that obtained by expression of the unmodified DNA in the organism in which the protein is endogenous.
34. DNA which is complementary to that which hybridizes under stringent conditions with the DNA of any one of claims 16 to 29.
35. A vector containing a DNA sequence as claimed in any one of claims 16 to 34.
36. Plant cell transformed with the DNA of any one of claims 16 to 34 or the vector of claim 35, which contains the DNA stably incorporated into its genome.

37. Plant cell according to claim 36, which is part of a whole plant.
38. Plants transformed with the DNA of any one of claims 16 to 34 or the vector of claim 35, the progeny of such plants which contain the DNA stably incorporated, and/or the apomictic seeds of such plants or such progeny.
39. Plants transformed with the DNA comprised by the recombinant DNA of claims 16 to 34.
40. Use of the DNA of any one of claims 16-34 in the manufacture of apomictic seeds.
41. Plants which are derived from apomictic seeds obtainable by the method of any one of claims 1-15 or 40.
42. A method of obtaining cultivars comprising the steps of fertilizing plants with the pollen of the plants of either of claims 38, 39 or 40 and cultivars which result from the said method.
43. A method of obtaining embryogenic cells in plant material, comprising transforming the material with a recombinant DNA sequence as claimed in any one of claims 16-34, the DNA comprised by the recombinant DNA of any one of claims 16 to 34, or the vector of claim 35, expressing the sequence in the material or derivatives thereof and subjecting the said material or derivatives to a compound which acts as a ligand for the gene product of the said sequence.
44. A method according to the preceding claim, wherein the sequence encodes a leucine rich repeat receptor like kinase, and the compound is a phyto-hormone.
45. A method of generating somatic embryos under *in vitro* conditions wherein the SERK protein is overexpressed ectopically.
46. A bag containing apomictic seeds obtainable by the method of any one of claims 1-15 or 40.

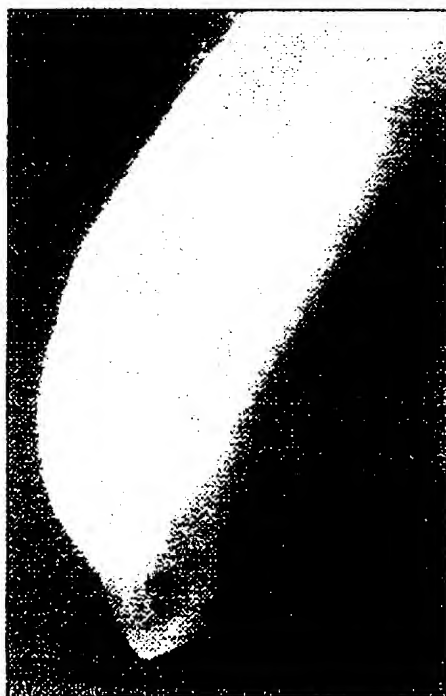
**Fig. 1**

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***Fig. 2***



**FIG. 2A**



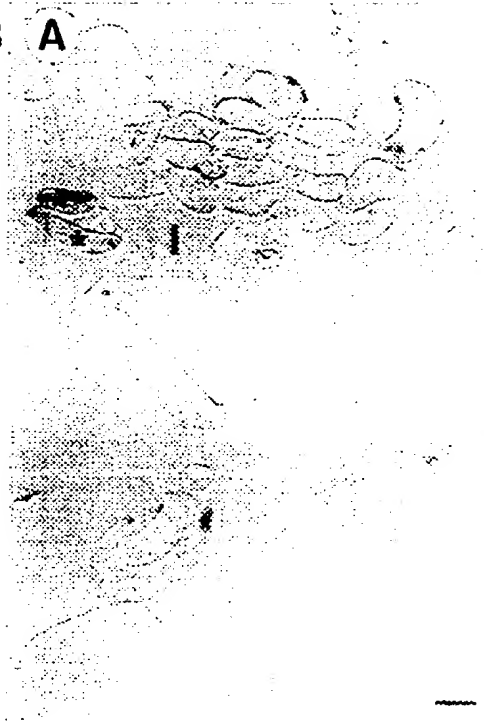
**FIG. 2B**

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***Fig. 3***

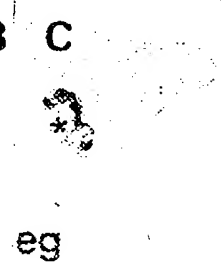
**FIG. 3 A**



**FIG. 3 B**

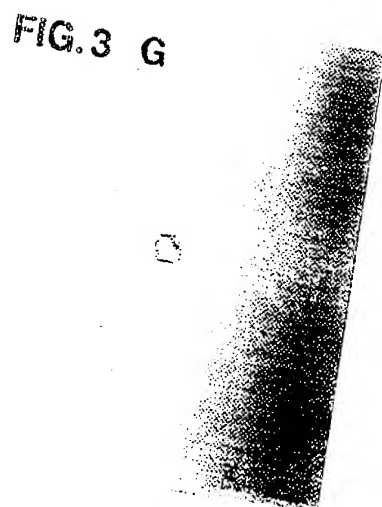
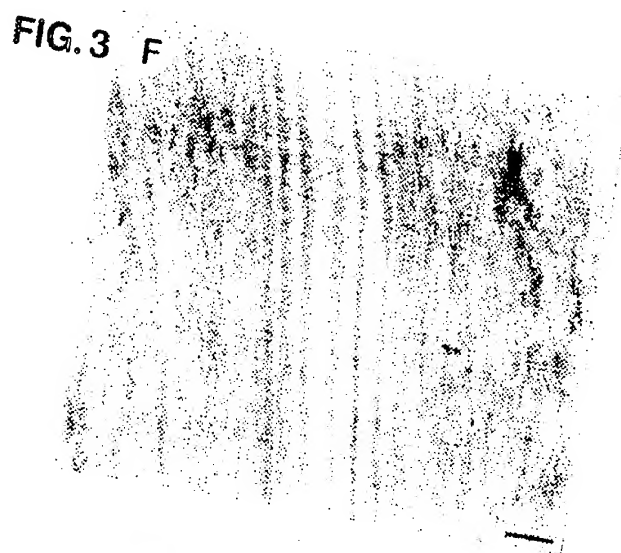
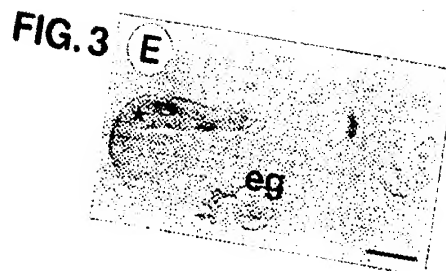
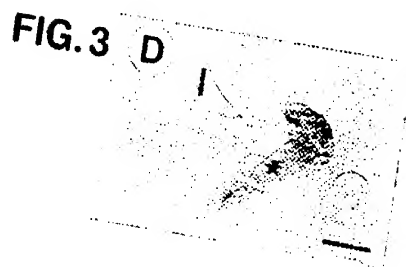


**FIG. 3 C**



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***Fig. 3*** (cont.)

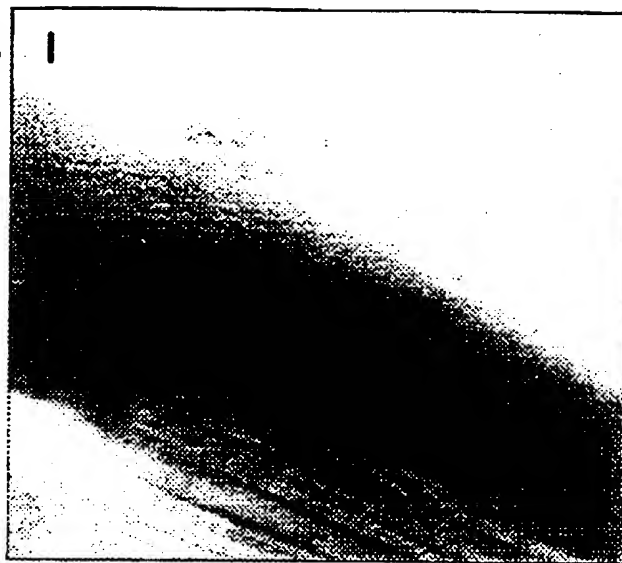


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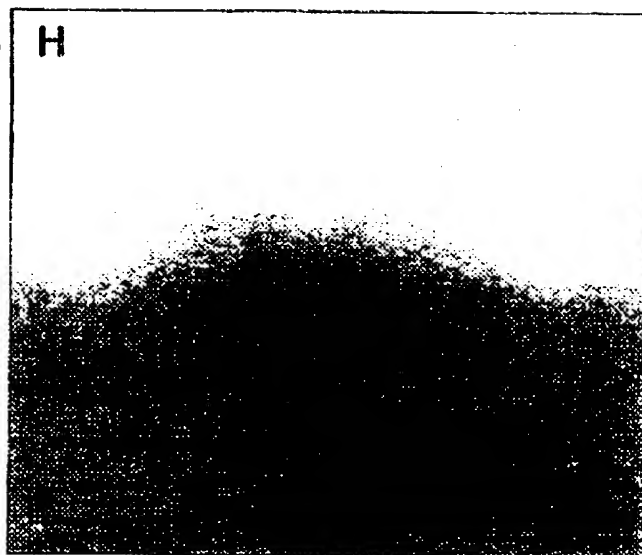
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***Fig. 3*** (cont.)

**FIG. 3 I**



**FIG. 3 H**



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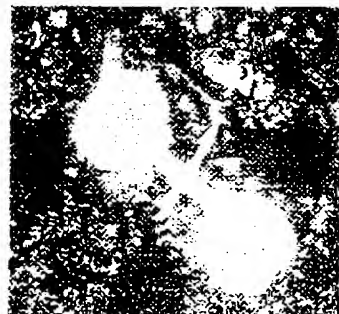
***Fig. 4***



no. I

no. II

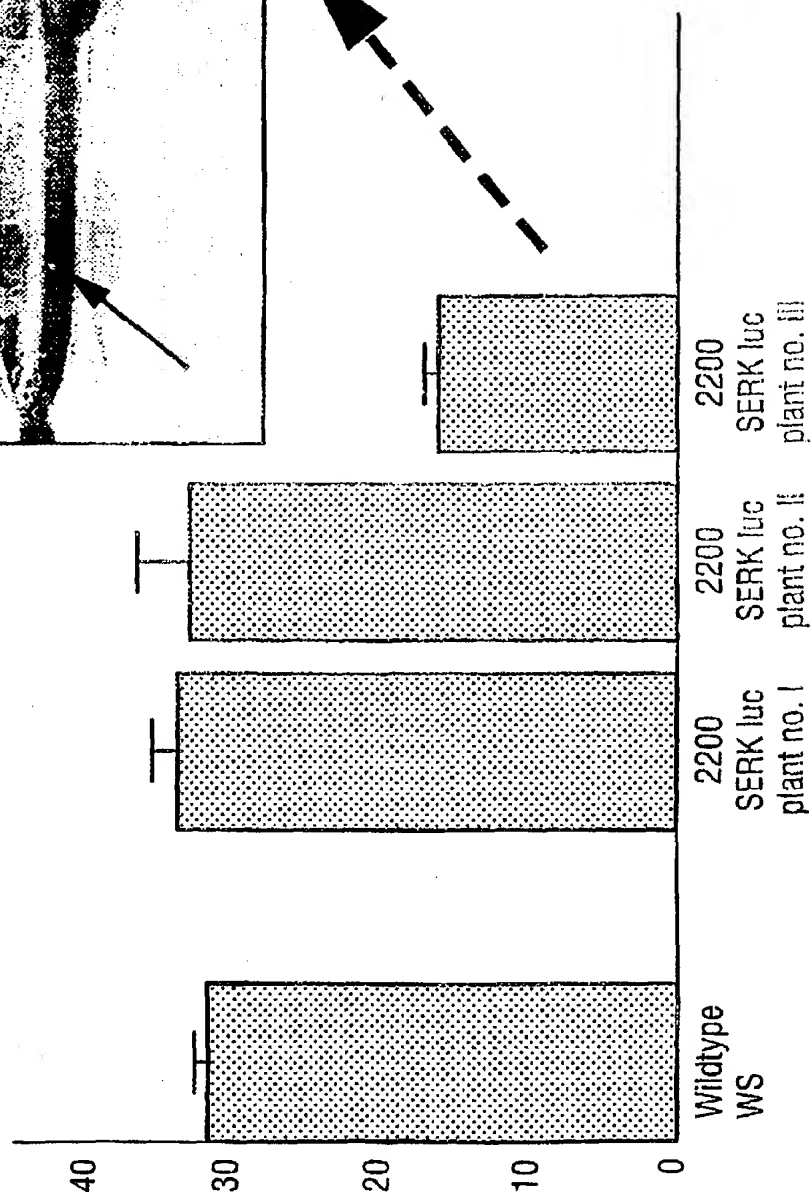
no. III



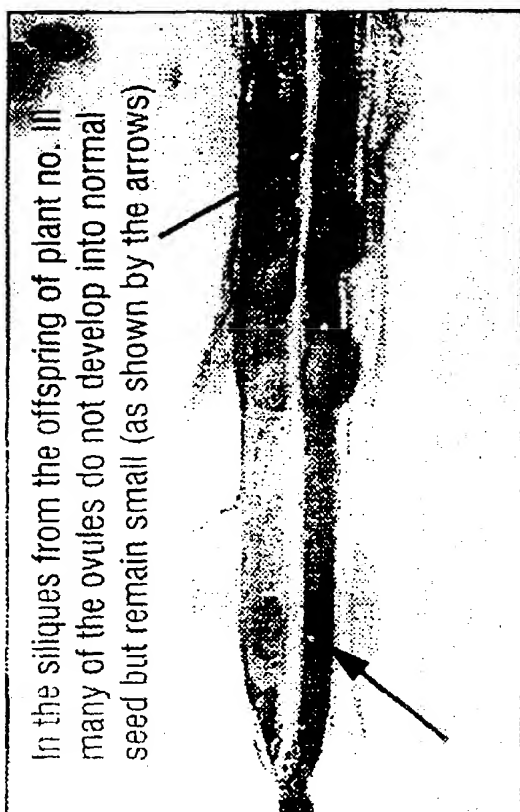
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**Fig. 5**

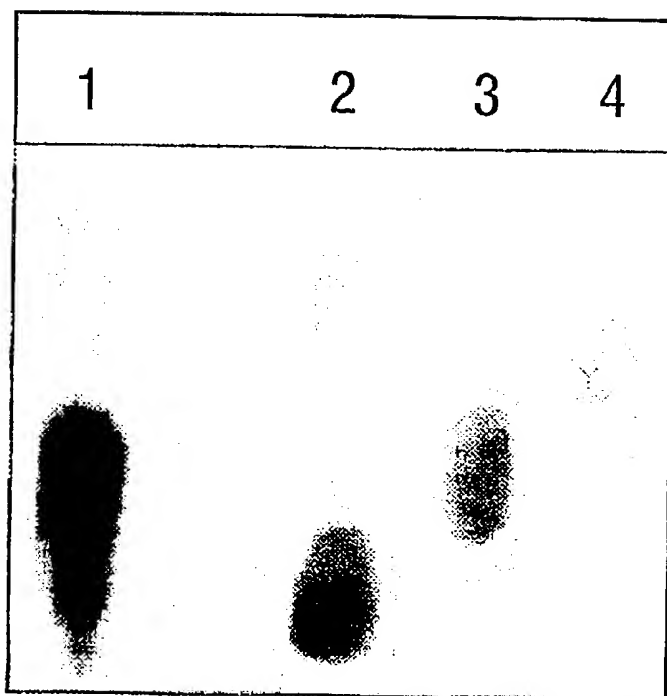
Developing green ovules average of  
four siliques from three T2 plants each



In the siliques from the offspring of plant no. III many of the ovules do not develop into normal seed but remain small (as shown by the arrows)



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***Fig. 6***

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# INTERNATIONAL SEARCH REPORT

International Application No  
PCT/EP 97/02443

A. CLASSIFICATION OF SUBJECT MATTER  
IPC 6 C12N15/82 C12N9/12 C07K14/415 A01H5/00

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)  
IPC 6 C12N A01H C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
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☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

### \* Special categories of cited documents:

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Date of the actual completion of the international search

17 September 1997

Date of mailing of the international search report

30.09.97

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Holtorf, S

## INTERNATIONAL SEARCH REPORT

International Application No

PCT/EP 97/02443

## C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

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International Application No  
PCT/EP 97/02443

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